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(54) Title: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE PROTEINS OF THERAPEUTIC POTENTIAL

(57) Abstract: A computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of computing the sequence-based attributes of a neural network software wherein the attributes are (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition, training the artificial neural Network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51 ; a computer system for performing the method; and genes and proteins encoding adhesin and adhesin-like proteins.



WO 2005/076010 A2

COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE PROTEINS OF THERAPEUTIC POTENTIAL

Field of the present Invention

5 A computational method for identifying adhesin and adhesin-like proteins; computer system for performing the method; and genes and proteins encoding adhesin and adhesin-like proteins

Background and prior art of the present invention

10 The progress in genome sequencing projects has generated a large number of inferred protein sequences from different organisms. It is expected that the availability of the information on the complete set of proteins from infectious human pathogens will enable us to develop novel molecular approaches to combat them. A necessary step in the successful colonization and subsequent manifestation of disease by microbial pathogens is the ability to adhere to host cells.

15 Microbial pathogens encode several proteins known as adhesins that mediate their adherence to host cell surface receptors, membranes, or extracellular matrix for successful colonization. Investigations in this primary event of host-pathogen interaction over the past decades have revealed a wide array of adhesins in a variety of pathogenic microbes. Presently, substantial information on the biogenesis of adhesins and the regulation of adhesin factors is available. One of the best understood mechanisms of bacterial adherence is attachment mediated by pili or fimbriae. Several afimbrial adhesins also have been reported. In addition, limited knowledge on the target host receptors also has been gained (Finlay, B.B. and Falkow, S 1997).

25 New approaches to vaccine development focus on targeting adhesins to abrogate the colonization process (Wizemann, *et al* 1999). However, the specific role of particular adhesins has been difficult to elucidate. Thus, prediction of adhesins or adhesin-like proteins and their functional characterization is likely to aid not only in deciphering the molecular mechanisms of host pathogen interaction but also in developing new vaccine formulations, which can be tested in suitable experimental model systems.

30 One of the best understood mechanisms of bacterial adherence is attachment mediated by pili or fimbriae. For example, FimH and PapG adhesins of *Escherichia coli* (Maurer, L., Orndorff, P.(1987), Bock, K., *et al.*(1985). Other examples of pili group adhesins include type IV pili in *Pseudomonas aeruginosa*, *Neisseria* species, *Moraxella* species, Enteropathogenic *Escherichia coli* and *Vibrio cholerae* (Sperandio V *et al* (1996).

Several afimbrial adhesins are HMW proteins of *Haemophilus influenzae* (van Schilfgaarde 2000), the filamentous hemagglutinin, pertactin, of *Bordetella pertussis* (Bassinet *et al* 2000), the BabA of *H. pylori* (Yu J *et al* 2002) and the YadA adhesin of *Yersinia enterocolitica* (Neubauer *et al* 2000). The intimin receptor protein (Tir) of Enteropathogenic *E. coli* (EPEC) is another type of adhesin (Ide T *et al* 2003). Other class of adhesins includes MrkD protein of *Klebsella pneumoniae*, Hia of *H. influenzae* (St Geme *et al* 2000), Ag I/II of *Streptococcus mutans* and SspA, SspB of *Streptococcus gordonii* (Egland *et al* 2001), FnbA, FnbB of *Staphylococcus aureus* and SfbI, protein F of *Streptococcus pyogenes*, the PsaA of *Streptococcus pneumoniae* (De
5 10 *et al* 2003).

A known example of adhesins approved as vaccine is the acellular pertussis vaccine containing FHA and pertactin against *B. pertussis* the causative agent of whooping cough (Halperin, S *et al* 2003). Immunization with FimH is being evaluated for protective immunity against pathogenic *E. coli* (Langermann S *et al* 2000), in
15 *Streptococcus pneumoniae*, PsaA is being investigated as a potential vaccine candidate against pneumococcal disease (Rapola, S *et al* 2003). Immunization results with BabA adhesin showed promise for developing a vaccine against *H. pylori* (Prinz, C *et al* 2003). A synthetic peptide sequence anti-adhesin vaccine is being evaluated for protection against *Pseudomonas aeruginosa* infections.

20 Screening for adhesin and adhesin like proteins by conventional experimental method is laborious, time consuming and expensive. As an alternative, homology search is used to facilitate the identification of adhesins. Although, this procedure is useful in the analysis of genome organization (Wolf *et al* 2001) and of metabolic pathways (Peregrin-Alvarez *et al* 2003, Rison *et al* 2002), it is somewhat limited in allowing
25 functional predictions when the homologues are not functionally characterized or the sequence divergence is high. Assignment of functional roles to proteins based on this technique has been possible for only about 60% of the predicted protein sequences (Fraser *et al* 2000). Thus, we explored the possibility of developing a non-homology method based on sequence composition properties combined with the power of the
30 Artificial Neural Networks to identify adhesins and adhesin-like proteins in species belonging to wide phylogenetic spectrum.

Twenty years ago, Nishikawa *et al* carried out some of the early attempts to classify proteins into different groups based on compositional analysis (Nishikawa *et al* 1983).

More recently, the software PropSearch was developed for analyzing protein sequences where conventional alignment tools fail to identify significantly similar sequences (Hobohm, U. and Sander, C 1995). PropSearch uses 144 compositional properties of protein sequences to detect possible structural or functional relationships between a new sequence and sequences in the database. Recently the compositional attributes of proteins have been used to develop softwares for predicting secretory proteins in bacteria and apicoplast targeted proteins in *Plasmodium falciparum* by training Artificial Neural Networks (Zuegge *et al* 2001).

Zuegge *et al* have used the 20 amino acid compositional properties. Their objective was to extract features of apicoplast targeted proteins in *Plasmodium falciparum*. This is distinct from our software SPAAN that focuses on adhesins and adhesin-like proteins involved in host-pathogen interaction.

Hobohm and Sander have used 144 compositional properties including isoelectric point and amino acid and dipeptide composition to generate hypotheses on putative functional role of proteins that are refractory to analysis using other sequence alignment based approaches like BLAST and FASTA. Hobohm and Sander do not specifically address the issue of adhesins and adhesin-like proteins, which is the focus of SPAAN

Nishikawa *et al* had originally attempted to classify proteins into various functional groups. This was a curiosity driven exercise but eventually lead to the development of a software to discriminate extra-cellular proteins from intracellular proteins. This work did not address the issue of adhesins and adhesin-like proteins, which is the focus of SPAAN.

Thus, none of the aforementioned research groups have been able to envisage the methodology of the instant application. The inventive method of this application provides novel proteins and corresponding gene sequences.

Adhesins and adhesin-like proteins mediate host-pathogen interactions. This is the first step in colonization of a host by microbial pathogens. Attempts Worldwide are focused on designing vaccine formulations comprising adhesin proteins derived from pathogens. When immunized, host will have its immune system primed against adhesins for that pathogen. When a pathogen is actually encountered, the surveillance mechanism will recognize these adhesins, bind them through antigen-antibody interactions and neutralize the pathogen through complement mediate cascade and other related clearance mechanisms. This strategy has been successfully employed in

the case of Whooping cough and is being actively pursued in the case of Pneumonia, Gastric Ulcer and Urinary tract infections.

Objects of the present Invention

The main object of the present invention is to provide a computational method for identifying adhesin and adhesin-like proteins of therapeutic potential.

Another object of invention is to provide a method for screening the proteins with unique compositional characteristics as putative adhesins in different pathogens.

Yet, another object of the invention is providing the use of gene sequences encoding the putative adhesin proteins useful as preventive therapeutics.

Summary of the present Invention

A computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of computing the sequence-based attributes of protein sequences using five attribute modules of software SPAAN, (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition, training the artificial neural Network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51 ; a computer system for performing the method; and genes and proteins encoding adhesin and adhesin-like proteins

Detailed description of the present Invention

Accordingly, the present invention relates to a computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of computing the sequence-based attributes of protein sequences using five attribute modules of software SPAAN, (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition, training the artificial neural Network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51 ; a computer system for performing the method; and genes and proteins encoding adhesin and adhesin-like proteins

In an embodiment of the present invention, wherein the invention relates to a computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of:

- a. computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, wherein the attributes

are software, (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition,

- b. training the artificial neural Network (ANN) for each of the computed five attributes, and
- c. identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51 .

In another embodiment of the present invention, wherein the invention relates to a method wherein the protein sequences is obtained from pathogens, eukaryotes, and multicellular organisms.

In an embodiment of the present invention, wherein the invention relates to a method, wherein the protein sequences are obtained from the pathogens selected from a group of organisms comprising *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Mycoplasma pneumoniae*, *Mycobacterium tuberculosis*, *Rickettsiae prowazekii*, *Porphyromonas gingivalis*, *Shigella flexneri*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Neisseria meningitides*, *Streptococcus pyogenes*, *Treponema pallidum* and Severe Acute Respiratory Syndrome associated human coronavirus (SARS).

In yet another embodiment of the present invention, wherein the method of the invention is a non-homology method.

In still another embodiment of the present invention, wherein the invention relates to the method using 105 compositional properties of the sequences.

In still another embodiment of the present invention, wherein the invention relates to a method showing sensitivity of at least 90%.

In still another embodiment of the present invention, wherein the invention relates to the method showing specificity of 100%.

In still another embodiment of the present invention, wherein the invention relates to a method identifying adhesins from distantly related organisms.

In still another embodiment of the present invention, wherein the invention relates to the neural network has multi-layer feed forward topology, consisting of an input layer, one hidden layer, and an output layer.

In still another embodiment of the present invention, wherein the invention relates to the number of neurons in the input layer are equal to the number of input data points for each attribute.

In still another embodiment of the present invention, wherein the invention relates to the "P_{ad}" is a weighted linear sum of the probabilities from five computed attributes.

In still another embodiment of the present invention, wherein the invention relates to each trained network assigns a probability value of being an adhesin for the protein sequence.

5 In still another embodiment of the present invention, wherein the invention relates to a computer system for performing the method of claim 1, said system comprising a central processing unit, executing SPAAN program, giving probabilities based on different attributes using Artificial Neural Network and in built other programs of assessing attributes, all stored in a memory device accessed by CPU, a display on
10 which the central processing unit displays the screens of the above mentioned programs in response to user inputs; and a user interface device.

In still another embodiment of the present invention, wherein the invention relates to a set of 274 annotated genes encoding adhesin and adhesin-like proteins, having SEQ ID
15 Nos. 385 to 658.

In still another embodiment of the present invention, wherein the invention relates to a set of 105 hypothetical genes encoding adhesin and adhesin-like proteins, having SEQ ID Nos. 659 to 763.

In still another embodiment of the present invention, wherein the invention relates to a set of 279 annotated adhesin and adhesin-like proteins of SEQ ID Nos. 1 to 279.

In still another embodiment of the present invention, wherein the invention relates to a set of 105 hypothetical adhesin and adhesin-like proteins of SEQ ID Nos. 280 to 384.

One more embodiment of the present invention, wherein the invention also relates to a fully connected multilayer feed forward Artificial Neural Network based on the
25 computational method as claimed in claim 1, comprising of an input layer, a hidden layer and an output layer which are connected in the said sequence, wherein each neuron is a binary digit number and is connected to each neuron of the subsequent layer for identifying adhesin or adhesin like proteins, wherein the program steps comprise:-
[a] feeding a protein sequence in FASTA format; [b] processing the sequence
30 obtained in step [a] through the 5 modules named A, C, D, H and M, wherein attribute A represents an amino acid composition, attribute C represents a charge composition, attribute D represents a dipeptide composition of the 20 dipeptides [NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI and HR], attribute H

represents a hydrophobic composition and attribute M represents amino acid frequencies in multiplets to quantify 5 types of compositional attributes of the said protein sequence to obtain numerical input vectors respectively for each of the said attributes wherein the sum of numerical input vectors is 105; [c] processing of the numerical input vectors obtained in step [b] by the input neuron layer to obtain signals, wherein the number of neurons is equal to the number of numerical input vectors for each attribute; [d] processing of signals obtained from step [c] by the hidden layer to obtain synaptic weighted signals, wherein the optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually; [e] delivering synaptic weighted signals obtained from step [d] to the output layer for assigning of a probability value for each protein sequence fed in step [a] as being an adhesin by each network module; [f] using the individual probabilities obtained from step [e] for computing the final probability of a protein sequence being an adhesin denoted by the P_{ad} value, which is a weighted average of the individual probabilities obtained from step [e] and the associated fraction of correlation which is a measure of the strength of the prediction.

In still another embodiment of the present invention, wherein the input neuron layer consists of a total of 105 neurons corresponding to 105 compositional properties.

In still another embodiment of the present invention, wherein the hidden layer comprises of neurons represented as 30 for amino acid frequencies, 28 for multiplet frequencies, 28 for dipeptide frequencies, 30 for charge composition and 30 for hydrophobic composition.

In still another embodiment of the present invention, wherein the output layer comprises of neurons to deliver the output values as probability value for each protein sequence.

Identification of novel adhesins and their characterization are important for studying host-pathogen interactions and testing new vaccine formulations. We have employed Artificial Neural Networks to develop an algorithm SPAAN (Software for Prediction of Adhesin and Adhesin-like proteins using Neural Networks) that can identify adhesin proteins using 105 compositional properties of a protein sequence. SPAAN could correctly predict well characterized adhesins from several bacterial species and strains. SPAAN showed 89% sensitivity and 100% specificity in a test data set that did not

contain proteins in the training set. Putative adhesins identified by the software can serve as potential preventive therapeutics.

The present invention provides a novel computational method for identifying adhesin and adhesin-like proteins of therapeutic potential. More particularly, the present invention relates to candidate genes for these adhesins. The invention further provides new leads for development of candidate genes, and their encoded proteins in their functional relevance to preventive approaches. This computational method involves calculation of several sequence attributes and their subsequent analyses lead to the identification of adhesin proteins in different pathogens. Thus, the present invention is useful for identification of the adhesin proteins in pathogenic organisms. The adhesin proteins from different genomes constitute a set of candidates for functional characterization through targeted gene disruption, microarrays and proteomics. Further, these proteins constitute a set of candidates for further testing in development of preventive therapeutics. Also, are provided the genes encoding the candidate adhesin proteins.

The present method offers novelty in the principles used and the power of Neural Networks to identify new adhesins compared to laborious and time consuming conventional methods. The present method is based on compositional properties of proteins instead of sequence alignments. Therefore this method has the ability to identify adhesin and adhesin like proteins from bacteria belonging to a wide phylogenetic spectrum. The predictions made from this method are readily verifiable through independent analysis and experimentation. The invention has the potential to accelerate the development of new preventive therapeutics, which currently requires high investment in terms of requirement of skilled labor and valuable time.

The present invention relates to a computational method for the identification of candidate adhesin proteins of therapeutic potential. The invention particularly describes a novel method to identify adhesin proteins in different genomes of pathogens. These adhesin proteins can be used for developing preventive therapeutics.

Accordingly, a computational method for identifying adhesin and adhesin-like proteins of therapeutic potential which comprises calculation of 105 compositional properties under the five sequence attributes, namely, Amino Acid frequency, Multiplet frequency, dipeptide frequency, charge composition and hydrophobic composition; and then training Artificial Neural Network (ANN, Feed Forward Error Back Propagation)

using these properties for differentiating between adhesin and non-adhesin class of proteins. This computational method involves quantifying 105 compositional attributes of query proteins and qualifying them as adhesins or non-adhesins by a P_{ad} value (Probability of being an adhesin). The present invention is useful for identification of adhesin and adhesin-like proteins in pathogenic organisms. These newly identified adhesin and adhesin-like proteins constitute a set of candidates for development of new preventive therapeutics that can be tested in suitable experimental model systems readily. In addition, the genes encoding the candidate adhesin and adhesin-like proteins are provided.

The invention provides a set of candidate adhesin and adhesin-like proteins and their coding genes for further evaluation as preventive therapeutics. The method of invention is based on the analysis of protein sequence attributes instead of sequence patterns classified to functional domains. Present method is less dependent on sequence relationships and therefore offers the potential power of identifying adhesins from distantly related organisms. The invention provides a computational method, which involves prediction of adhesin and adhesin-like proteins using Artificial Neural Networks. The proteins termed adhesin were found to be predicted with a high probability ($P_{ad} = 0.51$) in various pathogens. Some adhesin sequences turned out to be identical or homologous to proteins that are antigenic or implicated in virulence. By this approach, proteins could be identified and short-listed for further testing in development of new vaccine formulations to eliminate diseases caused by various pathogenic organisms.

DESCRIPTION OF TABLES

Table 1: Output file format given by SPAAN.

Table 2: Organism Name, Accession number, Number of base pairs, Date of release and Total number of proteins.

Table 3. Prediction of well characterized adhesins from various bacterial pathogens using SPAAN.

Table 4. Analysis of predictions made by SPAAN on genome scans of a few selected pathogenic organisms.

Table 5: GI numbers and Gene IDs of new putative adhesins predicted by SPAAN in the genomes listed in Table 2.

Table 6: GI numbers and Gene IDs of hypothetical proteins predicted as putative adhesins by SPAAN in the genomes listed in Table 2.

Table 7: The list of 198 adhesins found in bacteria

Brief description of the accompanying drawings

5 **Figure 1** shows the Neural Network architecture

Figure 2 shows assessment of SPAAN using defined test dataset.

Figure 3 (a) shows Histogram plots of the number of proteins in the various P_{ad} value ranges are shown. **(b)** Pairwise sequence relationships among the adhesins were determined using CLUSTAL W and plotted on X-axis. Higher scores indicate similar pairs. **(c)** plot for non-adhesins. Data are plotted in the 4 quadrant format for clear inspection.

Software program was written in C Language and operated on Red Hat Linux 8.0 operating system. The computer program accepts input protein sequences in FastA format and produces a tabulated output. The output Table contains one row for each protein listing the probability outputs of each of the five modules, a weighted average probability of these five modules (P_{ad}), and the function of the protein as described in the input sequence file. This software is called SPAAN (A Software for Prediction of Adhesins and Adhesin-like proteins using Neural Networks) and a software copyright has been filed. Although this software has multiple modules, the running of these modules have been integrated and automated. The user only needs to run one command.

AAcomp.c:

Input: File containing protein sequences in the fasta format.

Output: File containing frequencies of all 20 AAs for each protein in one row.

25 **charge.c:**

Input: File containing protein sequences in the fasta format.

Output: File containing frequency of charged amino acids (R, K, E and D) and moments (up to 18th order) of the positions of charged amino acids.

hdr.c:

30 **Input:** File containing protein sequences in the fasta format.

Output: File containing frequencies of 5 groups of amino acids formed on the basis their Hydrophobicity and moments of their positions up to 5th order.

multiplets.c:

Input: File containing protein sequences in the fasta format.

5 **Output:** File containing fractions of multiplets of each of the 20 amino acids.

querydipep.c:

Input: File.1 containing protein sequences in the fasta format.

File.2 containing list of the significant dipeptides in dipeptide analysis.

10 **Output:** File containing frequencies of the dipeptides listed in the input File.2 for each protein in the input File.1.

train.c:

Input: File containing following specifications –

- 15
1. Number of input and output parameters.
 2. Number of nodes in the hidden layers.
 3. Names of the training, validate and test data files.
 4. Learning rate, coefficient of moment.
 5. Maximum number of cycles for training.

Output: Outputs are as follows.

- 20
1. Output of the trained NN for the test data set.
 2. Values of the weight connections in the trained NN.
 3. Some extra information about training.

recognize.c:

Input: File containing following specifications –

- 25
1. Number of input and output parameters.
 2. Number of nodes in the hidden layers.
 3. Names of the query input file.
 4. Name of the file containing values of the weight connections for trained NN.
 5. Name of the output file.

30 **Output:** Outputs for the query entries calculated by the trained NN.

standard.c:

Input: File containing protein sequences in fasta format.

Output: File containing protein sequences in fasta format with all the new line characters removed lying within a sequence.

5 **filter.c:**

Input: File containing protein sequences in fasta format.

Output: File containing protein sequences from the input except those which are short in length (<50 AAs) and which contain any amino acid other than the 20 known amino acids.

10 ***The five attributes:***Amino Acid frequencies

Amino acid frequency $f_i = (\text{counts of } i^{\text{th}} \text{ amino acid in the sequence}) / l$; $i = 1 \dots 20$, l is the length of the protein.

Multiplet frequency

15 Multiplets are defined as homopolymeric stretches $(X)_n$ where X is any of the 20 amino acids and n is an integer > 2 . After identifying all the multiplets, the frequencies of the amino acids in the multiplets were computed as

$$f_i(m) = (\text{counts of } i^{\text{th}} \text{ amino acid occurring as multiplet}) / l$$

Dipeptide frequencies

20 The frequency of a dipeptide (i, j) $f_{ij} = (\text{counts of } ij^{\text{th}} \text{ dipeptide}) / (\text{total dipeptide counts})$; i, j ranges from 1 to 20.

It has been found that dipeptide repeats in proteins are important for functional expression of the clumping factor present on *Staphylococcus aureus* cell surface that binds to fibrinogen (Hartford *et al* 1999). Thus we included the dipeptide frequency module. The total number of dipeptides is 400. For optimal training of Neural Network, the ratio of total number of input vectors to the total number of weight connections must be around 2 to avoid over fitting (Andrea *et al*). Therefore, we identified the dipeptides whose frequencies in the adhesin data set (469 proteins, see database construction) were significantly different from that in the non-adhesin dataset (703 proteins) using *t-test*. The frequencies of top 20 dipeptides (when arranged in the descending order of the p-values of *t-test*), were fed to the Neural Network. These dipeptides were (using single letter IUPAC-IUB code) NG, RE, TN, NT, GT, TT, DE,

ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI, AND HR. With frequency inputs for 20 dipeptides and 28 neurons in the 2nd layer, the total number of weight connections is 588, and is in keeping with the criterion of avoiding over fitting.

Charge composition

- 5 The input frequency of charged amino acids (R, K, E and D considering the ionization properties of the side chains at pH 7.2) given by $f_c = (\text{counts of charged amino acids}) / l$. Further, information on the characteristics of the distribution of the charged amino acids in a given protein sequence was provided by computing the moments of the positions of the occurrences of the charged amino acids. Since moments characterize
- 10 the patterns of distribution such as skewness and kurtosis (sharpness of the peak) we have used them to represent the distribution patterns of the charged residues in the sequence.

The general expression to compute moments of a given order; say 'i' is

$M_r = r^{\text{th}}$ order moment of the positions of charged amino acids

$$15 \quad = \sum \frac{(X_i - X_m)^r}{N}$$

Where, X_m = mean of all positions of charged amino acids

X_i = position of i^{th} charged amino acid

N = number of charged amino acids in the sequence

- The moments 2nd to 19th order were used to train the ANN constituting a total 20 inputs
- 20 in addition to frequency of charged amino acids and the length of the protein. The upper limit of 19th order was set based on assessments of sensitivity and specificity on a small dataset of adhesins and non-adhesins. Moments of order greater than 19 were not useful in improvement of performance.

Hydrophobic composition

- 25 A given protein sequence was digitally transformed using the hydrophobic scores of the amino acids according to Brendel *et al.* (43). The scores for five groups of amino acids: (-8 for K, E, D, R), (-4 for S, T, N, Q), (-2 for P, H), (+1 for A, G, Y, C, W), (+2 for L, V, I, F, M).

Following inputs were given for each of the group

- 30 (a) $f_i = (\text{counts of } i^{\text{th}} \text{ group}) / (\text{total counts in the protein})$; i ranges from 1 to 5
- (b) $m_{ji} = j^{\text{th}}$ order moment of positions of amino acids in i^{th} group; j ranges from 2 to 5.

A total of 25 inputs representing the hydrophobic composition of a protein were fed to the Neural Network. The rationale for using moments was same as described in the section on charge composition inputs.

Taken together a total of 105 compositional properties of a given protein sequence were used to predict their adhesin characteristics.

The software PropSearch uses 144 compositional properties of protein sequences to detect possible structural or functional relationships between a new sequence and sequences in the database (Hobohm and Sander 1995). The approach defines protein sequence dissimilarity (or distance) as a weighted sum of differences of compositional properties such as singlet and doublet amino acid composition, molecular weight, isoelectric point (protein property search or PropSearch). Compositional properties of proteins have also been used for predicting secretory proteins in bacteria and apicoplast targeted proteins in *Plasmodium falciparum* (Zuegge, et al. 2001). The properties used here are statistical methods, principal component analysis, self-organizing maps, and supervised neural networks. In SPAAN, we have used 105 compositional properties in the five modules viz. Amino Acid frequencies, Multiplet frequencies, Dipeptide frequencies, Charge composition, Hydrophobic composition. The total of 105 properties used in SPAAN are 20 for Amino acid frequencies, 20 for Multiplets frequencies, 20 for Dipeptide frequencies (Top 20 significant dipeptides are used, based on *t-test*), 20 for Charge composition (frequency of charged amino acids (R, K, E and D) and moments of 2nd to 19th order), and 25 for Hydrophobic composition (Amino acids were classified into five groups (-8 for K, E, D, R), (-4 for S, T, N, Q), (-2 for P, H), (+1 for A, G, Y, C, W), (+2 for L, V, I, F, M). A total of 25 inputs consisted of the following: Frequency of each group, Moments of positions of amino acids in each group from 2nd to 5th order.

Neural Network

A feed forward error back propagation Neural Network was used. The program is a kind gift from Charles W. Anderson, Department of Computer Science, Colorado State University, Fort Collins, CO 80523, anderson@cs.colostate.edu

Neural Network architecture

The Neural Network used here has a multi-layer feed-forward topology. It consists of an input layer, one hidden layer and an output layer. This is a 'fully-connected' Neural Network where each neuron *i* is connected to each unit *j* of the next layer (Figure 1).

The weight of each connection is denoted by w_{ij} . The state I_i of each neuron in the input layer is assigned directly from the input data, whereas the states of hidden layer neurons are computed by the sigmoid function,

$$h_j = 1 / (1 + \exp -(w_{j0} + \sum w_{ij} I_i)),$$

5 where, w_{j0} is the bias weight

The back propagation algorithm was used to minimize the differences between the computed output and the desired output. Ten thousand cycles (epochs) of iterations are performed. Subsequently, the best epoch with minimum error was identified. At this point the network produces approximate target values for a given input in the training set.

A network was trained optimally for each attribute. Thus five networks were prepared. The schematic diagram (Figure 1) shows the procedure adopted. The number of neurons in the input layer was equal to the number of input data points for each attribute (for example 20 neurons for 20 numerical input vectors of the amino acid composition attribute). The optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually. An upper limit for the total number of weight connections was set to half of the total number of input vectors to avoid over fitting as suggested previously (Andrea *et al*).

20 Computer programs to compute individual compositional attributes were written in C and executed on a PC under Red Hat Linux ver 7.3 or 8.0. The network was trained on the training set, checks error and optimizes using the validate set through back propagation. The validate set was different from the training set. Since, the number of well annotated adhesins were not many, we used the 'validate set' itself as test set for preliminary evaluation of the performance and to obtain the fraction of correlation to compute the weighted average probability (P_{ad} value) described in the next section. The training set had 367 adhesins and 580 non-adhesins. The validate set had 102 adhesins and 123 non-adhesins. The adhesins were qualified with a digit '1' and the non-adhesins were qualified with a digit '0'.

30 During predictions, the network is fed with new data from the sequences that were not part of training set. Each network assigns a probability value of being an adhesin to a given sequence. The final probability is computed as described in the next section.

Probability of being an adhesin, the P_{ad} value

Query proteins are processed modularly through network trained for each attribute. Thus, five probability outputs are obtained. Final prediction was computed using the following expression which is a weighted linear sum of the probabilities from five modules:

5

$$P_{ad} = \frac{(P_A * fc_A + P_C * fc_C + P_D * fc_D + P_H * fc_H + P_M * fc_M)}{(fc_A + fc_C + fc_D + fc_H + fc_M)}$$

P_i = Probability from i module,

fc_i = fraction of correlation of i module of the trained Neural Network,

Where i = A (Amino acid frequencies), C (Charge composition), D (Dipeptide
10 frequencies), H (Hydrophobic composition), or M (Multiplet frequencies).

The fraction of correlation fc_i represents the fraction of total entries that were correctly predicted ($P_{i,adhesin} > 0.5$ and $P_{i, non-adhesin} < 0.5$) by the trained network on the test set used in preliminary evaluation (Charles Anderson).

Neural Network

15 A feed forward error back propagation Neural Network was used. The program was downloaded from the web site with permission from the author, Charles W. Anderson, Department of Computer Science, Colorado State University, Fort Collins, CO 80523, anderson@cs.colostate.edu

Statistical Analysis

20 All statistical procedures were carried out using Microsoft Excel (Microsoft Corporation Inc. USA).

Sequence analysis

Homology analysis was carried out using CLUSTAL W (Thompson *et al* 1994), BLAST (Altschul *et al* 1990), CDD (conserved domain database) search (Marchler-
25 Bauer *et al* 2002).

The whole genome sequences of microbial pathogens present new opportunities for the development of clinical applications such as diagnostics and vaccines. The present invention provides new leads for the development of candidate genes, and their encoded proteins in their functional relevance to preventive therapeutics.

30 The protein sequences of both the classes, i.e. adhesin and non-adhesin, were downloaded from the existing database (National Centre for Biotechnology Information (NCBI), USA). A total of 105 compositional properties under the five sequence

attributes namely, amino acid composition, multiplet composition, dipeptide composition, charge composition and hydrophobic composition were computed by computer programs written in C language. The attributes were computed for all the proteins in both the databases. The sequence-based attributes were then used to train Artificial Neural Network for each of the protein attributes. Adhesins were qualified by the digit '1' and non-adhesins were qualified by the digit '0'. Finally each trained Artificial Neural Network was used to identify potential adhesins which can be envisaged to be useful for the development of preventive therapeutics against pathogenic infections. Accordingly, the invention provides a computational method for identifying adhesin and adhesin-like proteins of therapeutic potential, which comprises:

1. preparing two comprehensive data-sets of adhesin and non-adhesin proteins from publicly available information on protein sequences,
2. calculating computationally the sequence based attributes of the protein sequences in the publicly available protein datasets using specially developed Software for Prediction of Adhesins and Adhesin-like proteins using Neural Networks (SPAAN),
3. training the Artificial Neural Network (ANN) for the selected attributes,
4. assigning probability value suitable for an adhesin, " P_{ad} " to the query protein and identifying adhesin like property in the query proteins with the help of trained Artificial Neural Network implemented in SPAAN,
5. validating computationally the protein sequences as therapeutic potentials by comparing with the known protein sequences that are biochemically characterized in the pathogen genome.

In an embodiment of the invention the protein sequence data may be taken from an organism, specifically but not limited to organisms such as *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Mycoplasma pneumoniae*, *Mycobacterium tuberculosis*, *Rickettsiae prowazekii*, *Porphyromonas gingivalis*, *Shigella flexneri*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Neisseria meningitides*, *Streptococcus pyogenes*, *Treponema pallidum*, Severe Acute Respiratory Syndrome associated coronavirus.

In another embodiment to the present invention different sequence-based attributes used for identification of proteins of therapeutic potential, comprise amino acid composition, charge composition, hydrophobicity composition, multiplets frequencies, and dipeptide frequencies.

In an embodiment, the non-homologous adhesin protein sequence may be compared with that of known sequences of therapeutic applications in the selected pathogens.

In an embodiment of the invention, the sequences of adhesin or adhesin like proteins comprise sequences of sequences IDs listed in Tables 5 and 6 identified by the method
5 of invention.

.Another embodiment of the invention the computer system comprises a central processing unit, executing SPAAN program, giving probabilities based on different attributes using Artificial Neural Network and in built other programs of assessing attributes, all stored in a memory device accessed by CPU, a display on which the
10 central processing unit displays the screens of the above mentioned programs in response to user inputs; and a user interface device.

In One embodiment of the present invention, the particulars of the organisms such as their name, strain, accession number in NCBI database and other details are given in Table 2:

15 The invention is further explained with the help of the following examples, which are given by illustration and should be construed to limit the scope of the present invention in any manner.

Example 1

Operating SPAAN:

20 The purpose of the program is to computationally calculate various sequence-based attributes of the protein sequences.

The program works as follows:

The internet downloaded FASTA format files obtained from <http://www.ncbi.nlm.nih.gov> were saved by the name <organism_name>.faa are
25 converted in the standard format by C program and passed as input to another set of C programs which computes the 5 different attributes of protein sequences (a total of 105 compositional properties in all 5 modules).

The computed properties were fed as input to the 5 different Neural Networks. Each trained network assigns a probability value of being an adhesin for a query protein. The
30 final probability (P_{ad}) was calculated as weighted average of these five individual probabilities. The weights were determined from a correlation value of correct prediction during test runs of each of the five modules.

Input/Output format:**Downloaded Files and their format:**

<organism_name>.faa: file which stores the annotation and the protein sequence.

Input file Format: FASTA

5 ">gi.vertline."<annotation>

For example,

>gi.vertline.2314605.vertline.gb.vertline.AAD08472.vertline.histidine and glutamine-rich protein

MAHHEQQQQQQANSQHSHHHHHHAHHHHYYGGEHHHHNAQQHAEQQAEQQ
10 AQQQQQQQAHQQQQQKAQQQNQQY

>gi.vertline.3261822.vertline.gn1.vertline.PID.vertline.e328405 PE_PGRS

MIGDGANGGPGQPGGPGGLLYGNGGHGGAGAAGQDRGAGNSAGLIGNGGAG
GAGGNGGIGGAGAPGGLGGDGGKGGFADEFTGGFAQGGRRGGFGGNGNTGAS
GGMGGAGGAGGAGGAGGLLIGDGGAGGAGGIGGAGGVGGGGGAGGTGGGG
15 VASAFGGGNAFGGRGDDGGDGGTGGAGGARGAGGAGGAGGWLSGHSG
AHGAMGSGEGGAGGGGGARGEAGAGGGTSTGTNPGKAGAPGTQGDSGDP
GPPG

>gi.vertline... .

Table 1: Output file format given by SPAAN

20 <organism_name>.out

SN	P _A	P _C	P _D	P _H	P _M	P _{ad} -value	Protein Name
1	0.05683	0.290803	0.441338	0.50304	0.029503	0.260485	>gi.vertline.32454344.vert line.gb.vertline.AAP82966 .1. vertline.orfla polyprotein [SARS coronavirus Hong Kong ZY-2003]
2	0.639235	0.166721	0.054583	0.935385	0.453498	0.462452	>gi.vertline.32454345.vert line.gb.vertline.AAP82967 .1. vertline.orflab polyprotein [SARS coronavirus Hong Kong ZY-2003]
3	0.65111 1	0.91150 4	0.43869 6	0.54394 4	0.92404 4	0.690247	>gi.vertline.32454346.vert line.gb.vertline.AAP82968 .1. vertline.spike glycoprotein [SARS coronavirus Hong Kong ZY-2003]

4	0.464324	0.655003	0.179503	0.008700	0.241573	0.300970	>gi.vertline.32454347.vert line.gb.vertline.AAP82969 .1. vertline.Orf3a [SARS coronavirus Hong Kong ZY-2003]
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Where P_A , P_C , P_D , P_H , P_M are the outputs of the five Neural Networks.

Example 2 organisms and sequence numbers

Table 2: Organism Name, Accession number, Number of base pairs, Date of release
5 and Total number of proteins analyzed

Organism Name	Accession Number	Number of base pairs	Date of release	Total no. of proteins
<i>E. coli</i> O157 H7	NC_002695	5498450	7-Mar-2001	5361
<i>H. influenzae</i> Rd	NC_000907	1830138	30-Sep-1996	1709
<i>H. pylori</i> J99	NC_000921	1643831	10-Sep-2001	1491
<i>M. pneumoniae</i>	NC_000912	816394	2-Apr-2001	689
<i>M. tuberculosis</i> H37Rv	NC_000962	4411529	7-Sep-2001	3927
<i>R. prowazekii</i> strain Madrid E	NC_000963	1111523	10-Sep-2001	835
<i>P. gingivalis</i> W83	NC_002950	2343476	9-Sep-2003	1909
<i>S. flexneri</i> 2a str. 2457T	NC_004741	4599354	23- Apr-2003	4072
<i>S. mutans</i> UA159	NC_004350	2030921	25-Oct-2002	1960
<i>S. pneumoniae</i> R6	NC_003098	2038615	6-Sep-2001	2043
<i>N. meningitidis</i> serogroup A strain Z2491	NC_003116	2184406	27-Sep-2001	2065
<i>S. pyogenes</i> MGAS8232	NC_003485	1895017	Jan 31, 2002	1845
<i>T. pallidum</i> subsp. pallidum str. Nichols	NC_000919	1138011	7-Sep-2001	1036
Severe Acute Respiratory Syndrome (SARS) associated coronavirus Frankfurt 1	AY291315	29727	11-JUN-2003	14
SARS coronavirus HSR 1	AY323977	29751	15-OCT-2003	14

<i>SARS coronavirus</i> ZJ01	AY29702 8	29715	19-MAY-2003	3
<i>SARS coronavirus</i> TW1	AY29145 1	29729	14-MAY-2003	11
<i>SARS coronavirus</i> CUHK-Su10	AY28275 2	29736	07-MAY-2003	4
<i>SARS coronavirus</i> Urbani	AY27874 1	29727	12-AUG-2003	12
<i>SARS coronavirus</i>	NC_0047 18	29751	9-Sep-2003	29
<i>SARS coronavirus</i> Tor2	AY27411 9	29751	16-MAY-2003	15
<i>SARS coronavirus</i> GD01	AY27848 9	29757	18-AUG-2003	12
<i>SARS coronavirus</i> CUHK-W1	AY27855 4	29736	31-JUL-2003	11
<i>SARS coronavirus</i> BJ01	AY27848 8	29725	01-MAY-2003	11

Example 3

The multi-layered feed forward Neural Network architecture implemented in SPAAN (figure 1). A given protein sequence in FASTA format is first processed through the 5 modules A, C, D, H, and M to quantify the five types of compositional attributes. A: Amino acid composition, C: Charge composition, D: dipeptide composition of the 20 dipeptides (NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI, HR), H: Hydrophobic composition, M: Amino acid frequencies as Multiplets. The sequence shown is part of the FimH precursor (gi 5524634) of *E. coli*. Subsequently, these numerical data are input to the input neuron layer. The directions of arrows show data flow. The number of neurons chosen in the input layer was equal to the number of the numerical input vectors of each module. The network was optimally trained through minimization of error of detection based on validate set through back propagation. The details are described in the methods. Each network module assigns a probability value of the protein being an adhesin based on the corresponding attribute. The final probability of a protein sequence being an adhesin is the P_{ad} value a weighted average of the individual probabilities and the associated fraction of correlation which is a measure of the strength of the prediction.

Example 4

Performance of SPAAN assessed using a test set of 37 adhesins and 37 non-adhesins that were not part of the training set. Matthew's correlation coefficient (Mcc, plotted on

Y-axis) for all the proteins with P_{ad} values above a given threshold (plotted on X-axis) (figure 2). The Matthew's correlation is defined as:

$$Mcc = \frac{(TP * TN) - (FP * FN)}{\sqrt{(TN + FN)(TN + FP)(TP + FN)(TP + FP)}}$$

Where TP = True Positives, TN = True Negatives, FP = False Positives, FN = False
5 Negatives.

Here TPs are adhesins, TNs are non-adhesins. In general, adhesins have high P_{ad} value, whereas non-adhesins have low P_{ad} value. Thus known adhesins with P_{ad} value above a given threshold are true positives whereas known non-adhesins with P_{ad} value below the given threshold are true negatives. The sensitivity, Sn is given by $\left(\frac{TP}{TP + FN}\right)$ and

10 specificity, Sp is given by $\left(\frac{TN}{TN + FP}\right)$. False negatives are those cases, wherein a

known adhesin had P_{ad} value lower than the chosen threshold. Similarly, a known non-adhesin with a P_{ad} value higher than the chosen threshold was taken as false positive. A theoretical polynomial curve of second order (dashed line) was fitted to the observed curve (smooth line) with a Karl-Pearson correlation coefficient $R^2 = 0.9799$. The
15 maximum point of the theoretical curve (where first derivative vanishes and second derivative is negative) was chosen as reference (vertical dotted line) to identify the maximum $Mcc = 0.94$ on the observed curve (shown by arrow). The corresponding P_{ad} value threshold was 0.51. At this P_{ad} value threshold, Sn and Sp were 0.89 and 1.0 respectively. Note that the Mcc does not drop down to the x-axis because the highest
20 P_{ad} value attained by adhesins was 0.939 in comparison to the theoretical attainable limit of 1.0.

Example 5

Assessment of SPAAN on well known adhesins from various bacterial pathogens.

Table 3. Prediction of well characterized adhesins from various bacterial pathogens
25 using SPAAN.

Species	Disease caused	Adhesin ^a	Host ligand	P_{ad} value ^b (Range)
<i>E. coli</i>	Diarrhoea	PapG (27)	α -D-gal(1-4) β -D-Gal-containing receptors	0.84-0.76
		SfaS (5)	alpha-sialyl-beta-2,3-b-galactose	0.94-0.94
		FimH (63)	D-mannosides	0.96-0.23 ^c

		Intimin (12)	tyrosine-phosphorylated form of host cell receptor Hp90	0.95-0.78
		PrsG (5)	Gal(alpha1-4)Gal	0.86-0.85
Nontypeable <i>H. influenzae</i>	Influenza	HMW1, HMW2	Human epithelial cells	0.97
		Hia (8)	human conjunctival cells	0.93-0.90
<i>H. influenzae</i>	bacterial meningitis ^d	HifE (18)	Sialylganglioside-GM1	0.85-0.73
<i>K. pneumoniae</i>	Pneumonia	MrkD	type V collagen	0.82
<i>B. pertussis</i>	Whooping cough	FHA	Sulphated sugars on cell-surface glycoconjugates	0.85
		Pertactin	Integrins	0.43
<i>Y. enterocolitica</i>	Enterocolitis	YadA (5)	β_1 integrins	0.88-0.79
<i>S. mutans</i>	Dental Caries	SpaP (2)	Salivary glycoprotein	0.88, 0.87
		PAC	Salivary glycoprotein	0.88
<i>Streptococcus gordonii</i>	Oral cavity	SspA (2)	Salivary glycoprotein	0.85, 0.84
		CshA	Fibronectin	0.78
		CshB	Fibronectin	0.63
		ScaA	Co-aggregation	0.71
		SspB (2)	Salivary glycoprotein	0.85, 0.84
<i>Streptococcus sobrinus</i>	Tooth decay	SpaA	Salivary glycoprotein	0.89
		PAG (2)	Salivary glycoprotein	0.89, 0.73
<i>Streptococcus pyogenes</i>	Scarlet Fever	Protein F	Fibronectin	0.49
<i>Streptococcus pneumoniae</i>	Bacterial Pneumonia	PsaA (5)	Human nasopharyngeal cells	0.82-0.78
		CbpA ^e / SpsA / PbcA/ PspC	phosphorylcholine of the teichoic acid.	0.81-0.49
<i>Streptococcus parasanguis</i>	Valve endocarditis	FimA	Salivary glycoprotein fibrin	0.76
<i>Streptococcus sanguis</i>	Tooth Decay	SsaB	Salivary glycoprotein	0.71
<i>Enterococcus faecalis</i>	Empyema in patients with liver disease	EfaA	Unknown	0.83
<i>Staphylococcus aureus</i>	Food Poisoning	FnbA	Fibronectin	0.8
		FnbB (3)	Fibronectin	0.78, 0.77, 0.69
<i>Helicobacter pylori</i>	Peptic Ulcers	BabA (17)	difucosylated Lewis ^b blood group antigen	0.87-0.68

^a: The number of sequences from different strains and homologs from related species analyzed are shown in parantheses.

^b: Rounded off to the second decimal.

^c: Out of 63 FimH proteins, 54 were from *E. coli*, 6 from *Shigella flexneri*, 2 from *Salmonella enterica* and 1 was from *Salmonella typhimurium*. Except 2 FimH proteins, the rest had $P_{ad} = 0.51$. The 2 exceptions (gi numbers: 5524636, 1778448) were from *E. coli*. The gi:5524636 protein is annotated as a FimH precursor but is much shorter (129 amino acids) than other members of the family. The gi:1778448 protein is a *S. typhimurium* homolog in *E. coli*.

^d: Other ailments include pneumonia, epiglottitis, osteomyelitis, septic arthritis and sepsis in infants and older children.

^e: The adhesin CbpA is also known by alternative names SpsA, PbcA and PspC. A total of seven sequences were analyzed. Except 1 PspC sequence, the rest all had $P_{ad} = 0.51$.

Example 6

Ability of SPAAN to discriminate adhesins from non-adhesins at $P_{ad} = 0.51$ (figure 3-a).

Example 7

The non-homology character of SPAAN assesses in both adhesins and non-adhesins (figure 3b and 3c).

Figure 3 (a – c). SPAAN is non-homology based software. A total of 130 adhesins and 130 non-adhesins were analyzed to assess whether the predictive power of SPAAN could be influenced by the sequence relationships. (a) Histogram plots of the number of proteins in the various P_{ad} value ranges are shown. Shaded bars represent adhesins whereas open bars represent non-adhesins. Note the SPAAN's ability to segregate adhesins and non-adhesins into two distinct cohesive groups. (b) Pairwise sequence relationships among the adhesins were determined using CLUSTAL W and plotted on X-axis. Higher scores indicate similar pairs. The corresponding differences in P_{ad} values in the same protein pair was plotted on the Y-axis. Each point in the diagram represents a pair. Arrow points to protein pairs of the FimH family with high ΔP_{ad} values in spite of high similarity: Since one of the FimH proteins (gi: 5524636) had very low P_{ad} value all pairs with this false negative protein show high ΔP_{ad} values. The protein (gi: 5524636) is of much shorter length compared with other members of the same family. (c) plot for non-adhesins. Data are plotted in the 4 quadrant format for clear inspection. Note that among protein pairs with CLUSTAL W score < 20 the majority (82% in adhesins and 86% in non-adhesins) have $\Delta P_{ad} < 0.2$. These data support the non-homology character of SPAAN.

Example 8

Genomescan of pathogens by SPAAN identifies well known adhesins and new adhesins and adhesin-like proteins

Table 4. Analysis of predictions made by SPAAN on genome scans of a few selected

5 pathogenic organisms^a

Protein Class	Species	<i>Escherichia coli</i> O157:H7	<i>Mycobacterium tuberculosis</i> H37Rv	SARS associated corona virus (11 strains)
Total number of proteins with $P_{ad} \geq 0.51$		575	435	5
Known adhesins		17 ^b	-	-
Putative proteins with adhesin like characteristics		92 ^c	105 ^j	-
Hypothetical proteins with adhesin-like characteristics		22 ^d	-	-
Proteins likely to be extracytoplasmic or located at surface		190 ^e	191 ^k	5 ^m
Phage proteins		30 ^f	-	-
Others		13 ^g	6 ^l	-
Hypothetical proteins		157 ^h	86 ^h	-
Wrong predictions		54 ⁱ	47 ⁱ	-

^a: SPAAN has general applicability. The three pathogens chosen here are those in which intense investigations are being conducted presently. *M. tuberculosis* is of special importance to developing countries.

10 ^b: Fimbrial adhesins, AidA-I, gamma intimin, curlin, translocated intimin receptor, putative adhesin and transport, Iha, prepilin peptidase dependent protein C.

^c: These proteins have been annotated as proteins with a putative function. These sequences were analyzed using CDD (Conserved domain database, NCBI) and BLAST searches. Adhesin like domains were found in these proteins.

15 ^d: These proteins have been annotated as 'hypothetical'. These sequences were analyzed using CDD and BLAST searches. Adhesin like domains were found in these proteins.

^c: These proteins are outer membrane, extracellular, transport, surface, exported, flagellar, periplasmic lipoprotein, and proteins annotated as 'hypothetical' but found to have similar functions listed here using BLAST and CDD searches.

^d: The phage proteins were of the following functional roles – tail fiber, head
5 decoration, DNA injection, tail, major capsid, host specificity, endolysin.

^e: Proteins predicted by SPAAN but not readily classifiable into the classes listed here have been collectively grouped as 'Others'. However, some of these proteins are known to participate in host-pathogen interactions. The annotated functional roles are typeIII secretion, antibiotic resistance, heat shock, acid shock, structural, tellurium resistance,
10 terminase, Hcp-like, Sec-independent translocase, uncharacterized nucleoprotein, HicB-like.

^h: These proteins have been annotated as hypothetical. Re-analyses of these proteins using BLAST and CDD failed identify any function for these proteins.

ⁱ: These proteins have been annotated with functional roles that are very likely to occur
15 within the cell. Hence these proteins may have remote possibility of functioning as adhesins or adhesin-like proteins. Therefore this set of proteins have been incorrectly predicted as adhesins or adhesin-like by SPAAN.

^j: These proteins are PE_PGRS, PE proteins. Several reports (for example Brennan *et al.*) indicate that PE_PGRS proteins may be localized to cell surface and aid in host-
20 pathogen interaction.

^k: Lipoproteins (lpp, lpq, lpr), PPE, outer membrane, surface, transport, secreted, periplasmic, extracellular, ESAT-6, peptidoglycan binding, exported, mpt (with extracellular domains), and proteins annotated as 'hypothetical' but found to have similar functions listed here using BLAST and CDD searches.

^l: These proteins were of the following functions - glutaredoxin-like thioltransferase, putative involvement in molybdate uptake, ATP synthase chain, sulphotransferases, *S.erythraea* rhodanese-like protein M29612|SERCYSA_5, unknown function.
25

^m: These proteins were the spike glycoprotein with antigenic properties, and nsp2, nsp5, nsp6 and nsp7.

Table 5: New putative adhesins predicted by SPAAN in the genomes listed in table 2 –

(Total number = 279)

Protein GI Number	Gene ID	Protein name
<i>Escherichia coli</i> O157:H7		
13360742	912619	hemagglutinin/hemolysin-related protein
13362986	914770	putative ATP-binding component of a transport system
13361114	913228	putative tail fiber protein
13364757	913676	minor fimbrial subunit/D-mannose specific adhesin
13362687	915687	putative fimbrial-like protein
13360856	912599	AidA-I adhesin-like protein
13364140	915374	putative fimbrial protein
13359793	914435	putative invasin
13364768	913650	putative invasin
13364034	915471	Gamma intimin
13362703	915668	putative DNA transfer protein precursor
13364141	915376	putative fimbrial protein
13359819	914463	AidA-I adhesin-like protein
13360480	917768	putative fimbrial-like protein
13362692	915681	putative fimbrial-like protein
13362585	916824	putative ATP-binding component of a transport system
13359881	914526	putative flagellin structural protein
13361579	917311	putative type 1 fimbrial protein precursor
13360880	913991	curlin major subunit CsgA
13364036	915465	translocated intimin receptor Tir
13360740	912615	putative major pilin protein
13361582	917317	putative ATP-binding component of a transport system and adhesin protein
13364754	913683	export and assembly outer membrane protein of type 1 fimbriae
13360484	917767	homolog of Salmonella FimH protein

13364751	913688	major type 1 subunit fimbrin
13359597	913742	putative fimbrial protein
13362550	916787	putative ATP-binding component of a transport system
13359595	913739	putative fimbrial protein
13359599	913748	probable outer membrane porin protein involved in fimbrial assembly
13363900	915704	putative fimbrial protein precursor
13361575	917307	putative fimbrial-like protein
13364756	913678	fimbrial morphology
13363496	916142	truncated putative fimbrial protein
13359601	913761	putative fimbrial-like protein
13364145	915368	putative type 1 fimbrial protein
13363902	915708	putative outer membrane usher protein precursor
13361576	917309	putative outer membrane protein
13361013	913353	putative major tail subunit
13364755	913682	fimbrial morphology
13360738	912793	putative outer membrane usher protein
13363928	915608	alpha-amylase
13363495	916144	putative outer membrane protein
13362383	916617	putative type-1 fimbrial protein
13364373	914972	outer membrane vitamin B12 receptor protein BtuB
13360879	912479	minor curlin subunit precursor CsgB
13360739	912756	putative chaperone protein
13361574	917314	putative fimbrial-like protein
13361127	913212	outer membrane protease precursor
13363210	916442	putative lipoprotein
13361104	913238	major tail protein
13361709	917446	putative major tail subunit
13359725	914366	outer membrane pore protein PhoE
13360875	913765	curli production assembly/transport component CsgF
13362170	913927	putative outer membrane protein
13361473	917203	putative BigB-like protein

13364025	915286	EspF protein
13360081	916982	outer membrane receptor for ferric enterobactin (enterochelin) and colicins B and D
13362977	914779	hypothetical lipoprotein
13360351	917632	outer membrane protein X
13360696	914208	putative outer membrane precursor
13361456	917206	putative outer membrane protein
13361626	917374	putative outer host membrane protein precursor
13361698	917449	putative outer membrane protein
13362186	913421	putative outer membrane protein precursor
13362697	915676	long-chain fatty acid transport protein FadL
13360918	914188	flagellar hook protein FlgE
13360737	912506	putative outer membrane protein
13360342	917629	putative outer membrane receptor for iron transport
13363396	916248	outer membrane channel TolC
13361958	912705	putative scaffolding protein in the formation of a murein-synthesizing holoenzyme
13359921	914566	nucleoside-specific channel-forming protein TSX
13360944	913890	outer membrane receptor for ferric iron uptake
13359998	914644	putative outer membrane transport protein
13363390	916251	putative ferrichrome iron receptor precursor
13364227	915153	outer membrane phospholipase A
13361982	912846	putative outer membrane protein
13360129	917032	a minor lipoprotein
13361817	912692	putative outer membrane protein
13360233	917507	membrane spanning protein TolA
13362837	915218	putative outer membrane lipoprotein
13362328	912985	putative colanic acid biosynthesis glycosyl transferase

Haemophilus influenzae Rd

16272254	949521	prepilin peptidase-dependent protein D
16272928	950762	immunoglobulin A1 protease
16272129	951072	lipoprotein

16273251	950616	hemoglobin-binding protein
30995429	950130	opacity protein
16272854	949634	protective surface antigen D15
16272283	950648	opacity associated protein
16272604	949701	hemoglobin-binding protein
<i>Helicobacter pylori</i> J99		
4155101	889167	putative vacuolating cytotoxin (VacA) paralog
4154798	890022	putative vacuolating cytotoxin (VacA) paralog
4155426	890036	putative vacuolating cytotoxin (VacA) paralog
4155390	890075	vacuolating cytotoxin
4155400	890058	outer membrane protein - adhesin
4155681	889718	putative Outer membrane protein
4155420	890042	Outer membrane protein/porin
4155775	889799	outer membrane protein - adhesin
4155419	890044	Outer membrane protein/porin
4154526	889066	putative Outer membrane protein
4154724	889419	putative Outer membrane protein
4155862	890404	putative Outer membrane protein
4156048	889958	putative IRON(III) DICITRATE TRANSPORT PROTEIN
4154510	889297	putative Outer membrane protein
4155432	889515	putative outer membrane protein
4155623	889671	putative Outer membrane protein
4155700	889739	putative Outer membrane function
4154740	889426	Outer membrane protein/porin
4155692	889743	putative Outer membrane protein
4155594	889648	putative outer membrane protein
4155680	889719	putative Outer membrane protein
4155217	890243	putative Outer membrane protein
4155958	889905	putative Outer membrane protein
4155201	890259	putative Outer membrane protein
4155013	889232	cag island protein
4154974	889032	putative Outer membrane protein

4155214	890244	putative Outer membrane protein
4154973	889042	Outer membrane protein
4155344	890115	putative Outer membrane protein
4155099	889160	FLAGELLIN A
4155023	888978	cag island protein
4155035	889201	cag island protein, CYTOTOXICITY ASSOCIATED IMMUNODOMINANT ANTIGEN
4155289	890164	NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ PRECURSOR

Mycoplasma pneumoniae

13507881	877207	involved in cytodherence
13507880	877268	ADP1_MYCPN adhesin P1
13508228	877211	species specific lipoprotein
13508181	877124	species specific lipoprotein
13508179	877071	Mollicute specific lipoprotein, MG307 homolog, from M. genitalium
13508178	877118	Mollicute specific lipoprotein, MG307 homolog, from M. genitalium,
13508176	876797	Mollicute specific lipoprotein, MG307 homolog, from M. genitalium
13508175	876848	Mollicute specific lipoprotein, MG307 homolog, from M. genitalium
13508106	876953	involved in cytodherence
13508350	877112	similar to phosphate binding protein Pst

Mycobacterium tuberculosis H37 Rv

15607496	886491	PPE
15607445	886592	PPE
15610644	888270	PE_PGRS
15608588	886605	PE_PGRS
15609627	887941	PE_PGRS
15610643	888256	PE_PGRS
15607718	887725	PE_PGRS

15609054	885362	PPE
15610486	888113	PPE
15610483	888120	PPE
15610479	888033	PPE
15609771	888573	PE_PGRS
15610648	888306	PE_PGRS
15610481	888114	PE_PGRS
15608117	885264	PE_PGRS
15607973	885391	PE_PGRS
15608231	885258	PE_PGRS
15608906	885429	PE_PGRS
15608891	885544	PPE
15609990	888171	PE_PGRS
15609055	885506	PPE
15608227	887094	PE_PGRS
15610524	888151	PE_PGRS
15609490	886003	PPE
15607886	888664	PE_PGRS
15609624	887909	PE_PGRS
15607420	886621	PE_PGRS
15608897	885325	PE_PGRS(wag22)
15608590	886595	PE_PGRS
15609728	887992	PE_PGRS
15608012	885742	PE_PGRS
15608534	886745	PE_PGRS
15608940	885730	PE_PGRS
15607887	888662	PE_PGRS
15609235	888312	PE_PGRS
15610694	887822	PPE
15609533	885517	PE_PGRS
15610480		PE_PGRS

Rickettsia prowazekii strain Madrid E

15604316 883411 CELL SURFACE ANTIGEN (sca3)

15604546 883694 CELL SURFACE ANTIGEN (sca5)

Porphyromonas gingivalis W83

34541453 2551934 hemagglutinin protein HagA

34540040 2551409 lipoprotein, putative

34540364 2552375 extracellular protease, putative

34541613 2552074 hemagglutinin protein HagE

34540183 2551891 internalin-related protein

Shigella flexneri 2a str. 2457T

30065424 1080663 minor fimbrial subunit, D-mannose specific adhesin

30062726 1077662 putative adhesion and penetration protein

30063758 1078834 putative fimbrial-like protein

30065431 1080671 major type 1 subunit fimbrin (pilin)

30063366 1078379 flagellar protein FlhD

30064308 1079668 outer membrane fluffing protein

30062613 1077555 flagellar hook protein FlgE

30061954 1076843 conserved hypothetical lipoprotein

30065173 1080393 putative lipase

30065425 1080664 minor fimbrial subunit, precursor polypeptide

30064485 1079637 putative fimbrial protein

30062615 1077558 flagellar basal body L-ring protein FlgH

30064307 1079452 outer membrane fluffing protein

30065601 1080859 putative glycoprotein/receptor

30062118 1077025 putative fimbrial-like protein

30064099 1079223 lipoprotein

30062616 1077559 flagellar basal body P-ring protein FlgI

30063546 1078596 putative fimbrial-like protein

30062940 1077910 putative outer membrane protein

30065426 1080665 minor fimbrial subunit, precursor polypeptide

30062779 1077721 putative outer membrane protein

30064194 1079329 putative lipoprotein

30063365 1078378 flagellin

30062298	1077222	outer membrane protein X
30064968	1080175	putative major fimbrial subunit
30061858	1076740	outer membrane pore protein E (E,Ic,NmpAB)
30062178	1080410	minor lipoprotein
30062479	1077412	putative fimbrial-like protein
30062565	1077506	minor curlin subunit precursor
30063880	1078972	putative outer membrane lipoprotein
30064531	1079686	cytoplasmic membrane protein
30065033	1080243	putative receptor protein
<i>Streptococcus mutans</i> UA159		
24378550	1029610	putative secreted antigen GbpB/SagA; putative peptidoglycan hydrolase
24379087	1028055	cell surface antigen SpaP
24380463	1029310	putative membrane protein
24379075	1028046	penicillin-binding protein 2b
24378955	1027967	penicillin-binding protein 1a; membrane carboxypeptidase
24379801	1028662	glucan-binding protein C, GbpC
24379528	1029536	hypothetical protein; possible cell wall protein, WapE
24379231	1028158	putative glucan-binding protein D; BglB-like protein
24380488	1029325	conserved hypothetical protein; possible transmembrane protein
24380291	1029139	putative amino acid binding protein
24379342	1028247	putative penicillin-binding protein, class C; fnt-like protein
24380047	1028904	putative ABC transporter, branched chain amino acid-binding protein
24378698	1029755	putative ABC transporter, metal binding lipoprotein; surface adhesin precursor; saliva-binding protein; lipoprotein receptor LraI (LraI family)
24378708	1029768	putative transfer protein
24379427	1028331	cell wall-associated protein precursor WapA
24379272	1028196	putative amino acid transporter, amino acid-binding protein
24379641	1028511	putative ABC transporter, amino acid binding protein

Streptococcus pneumoniae R6

15902395	934801	Choline-binding protein
15902381	934810	Choline-binding protein F
15902165	932894	Surface protein pspA precursor
15904047	934859	Choline binding protein D
15904036	933487	Choline binding protein A
15903986	933069	Choline-binding protein
15903796	933669	Autolysin (N-acetylmuramoyl-L-alanine amidase)

Neisseria meningitidis Z2491

15794121	907145	putative membrane protein
15794144	907168	putative surface fibril protein
15793284	906275	truncated pilin
15793460	906456	IgA-specific serine endopeptidase
15793282	906273	fimbrial protein precursor (pilin)
15793337	906332	adhesin
15793253	906243	putative lipoprotein
15794356	907848	putative lipoprotein
15793684	906699	putative membrane protein
15793290	906281	truncated pilin
15793283	906274	truncated pilin
15793475	906471	haemoglobin-haptoglobin-utilization protein
15793406	906401	porin, major outer membrane protein P.I
15794985	907333	adhesin MafA2
15794344	907836	putative lipoprotein
15794622	908118	hypothetical outer membrane protein
15793599	906604	pilus-associated protein
15793763	906779	putative periplasmic binding protein

Streptococcus pyogenes MGAS8232

19745214	995235	putative secreted protein
19746570	994224	putative penicillin-binding protein 1a
19745593	994771	putative 42 kDa protein
19745813	993958	putative adhesion protein

19745225	994839	putative choline binding protein
19745828	995250	streptolysin S associated protein
19746229	995021	putative minor tail protein
19746909	994105	putative laminin adhesion
19745560	995061	putative cell envelope proteinase

Treponema pallidum subsp. *pallidum* str. Nichols

15639714	2611034	flagellar hook protein (flgE)
15639609	2611657	tpr protein J (tprJ)
15639111	2610909	tpr protein C (tprC)
15639125	2610968	tpr protein D (tprD)

SARS coronavirus

31581505		spike protein S [SARS coronavirus Frankfurt 1]
32187357		spike protein S [SARS coronavirus HSR 1]
32187342		spike glycoprotein [SARS coronavirus ZJ01]
30698329		putative spike glycoprotein S [SARS coronavirus TW1]
30421454		putative spike glycoprotein [SARS coronavirus CUHK-Su10]
30027620		S protein [SARS coronavirus Urbani]
29836496	1489668	E2 glycoprotein precursor; putative spike glycoprotein [SARS coronavirus]
30795145		spike glycoprotein [SARS coronavirus Tor2]
31416295		spike glycoprotein S [SARS coronavirus GD01]
30023954		putative E2 glycoprotein precursor [SARS coronavirus CUHK-W1]
30275669		spike glycoprotein S [SARS coronavirus BJ01]
29837498		3C-like proteinase nsp5-pp1a/pp1ab (3CL-PRO) [SARS coronavirus]
29837501		putative nsp8-pp1a/pp1ab [SARS coronavirus]
29837503		putative nsp10-pp1a/pp1ab; formerly known as growth-factor-like protein [SARS coronavirus]
29837502		putative nsp9-pp1a/pp1ab [SARS coronavirus]

Table 6: Hypothetical proteins predicted as putative adhesins by SPAAN in the genomes listed in table 2 –

(Total number of proteins = 105)

Protein GI Gene ID
number

Escherichia coli O157:H7

13363955	915578
13360000	914929
13362244	912369
13359999	914888
13361583	917316
13361172	913156
13361131	913207
13359780	914422
13360571	912499
13362197	912893
13362260	912399
13360947	913505
13361464	917196
13361635	917367
13362421	916655
13361463	917195

Haemophilus influenzae Rd

16272115	951058
30995442	950581

Helicobacter pylori J99

4155526	889586
4155712	889748
4155632	889684
4156035	889468
4155499	

Mycoplasma pneumoniae

13507870	877230
13508239	877245
13508109	876868
13508025	877084
13507838	876784
13507883	877183
13507871	877239
13507944	877056
13508241	876750
13507942	877055
13507840	877387
13507867	877242
13508201	877044
13507941	876985
13508114	877397

Mycobacterium tuberculosis H37Rv

15611014	886198
15610173	887320
15609513	885515
15608094	885411
15610958	886155
15607528	886436
15607678	887473
15609587	885760
15610708	887227
15609526	885246
15611033	886225
15609028	885094
15607730	887771
15609121	885813
15608255	885951

15608409 887039

15609124 885815

15607734 887797

Rickettsia prowazekii strain Madrid E

15604649 883964

15604322 883472

15604659 883996

15604417 883217

Porphyromonas gingivalis W83

34540233 2551594

Shigella flexneri 2a str. 2457T

30062687 1077638

30062956 1080449

30063681 1078754

30065435 1080675

30063891 1078983

30063211 1078195

30065233 1080463

30064387 1079531

30062638 1077590

30065236 1080466

30061839 1076721

Streptococcus mutans UA159

24378864 1029452

24380475 1029319

24380237 1029088

24379203 1028139

24380480 1029320

24379275 1029489

24379291 1028216

24379295 1028215

24379804 1028663

24379162	1029417
24378987	1029363
24379179	1028118
24379166	1028107
24378827	1029444
24380216	1029067

Streptococcus pneumoniae R6

15902140	932867
15903446	934616
15903916	934001
15903848	933609
15902832	934332
15902372	934804
15902152	932889

Neisseria meningitidis Z2491

15793668	906680
15794714	907603

Streptococcus pyogenes MGAS8232

19747011	993608
19747024	994165
19747012	994373
19746396	995057
19746651	993824
19745883	995045
19745912	994077

Treponema pallidum subsp. *pallidum* str. Nichols

15639844	2611061
15639720	2611059

Table 7: The list of 198 adhesins found in bacteria
PapG (*E. coli*)

12837502

7407201

7407207
7407205
147096
4240529
7407203
42308
7443327
78746
18265934
26111419
26250987
26109826
26249418
13506767
42301
78745
129622
147092
13506906
7407209
147080
281926
7407199
147100
78744

SfaS (E.coli)

477910
264035
42959
134449
96425

FimH (E.coli)

26251208
26111640
5524634
29422425
5524630
29422435
29422415
10946257
29422419
11120564
29422457
11120562
29422459
5524632
29422455
29422453
29422451
29422449
29422447
29422445
29422443
29422437
29422433
29422431
29422429
29422427
29422423
29422421
29422417
729494
1361011
1790775

3599571
29422441
12620398
29422439
5524628
1787779
1742472
1742463
15801636
25321294
12515169
11120566
24051859
24112911
13360484
15800801
15830279
25392018
25500156
12514120
1787173
16128908
16501811
16759519
24051219
24112354
30040724
30062478
6650093
5524636
1778448

Intimin (E.coli)

	17384659
	4388530
	1389879
	15723931
	4323336
	4323338
	4323340
	4323342
	4323344
	4323346
	4323348
	4689314
PrsG (E.coli)	
	42523
	42529
	7443328
	7443329
	1172645
HMW1 (Nontypeable <i>H. influenzae</i>)	
	282097
HMW2 (Nontypeable <i>H. influenzae</i>)	
	5929966
Hia (Nontypeable <i>H. influenzae</i>)	
	25359682
	25359489
	25359709
	25359628
	25359414
	25359389
	21536216
	25359445
HifE (<i>H. influenzae</i>)	

	<i>13506868</i>
	13506870
	13506872
	13506874
	13506876
	3688787
	3688790
	3688793
	2126301
	1170264
	1170265
	533127
	535169
	3025668
	3025670
	3025672
	3025674
	642038
MrkD (<i>K. pneumoniae</i>)	
	<i>127307</i>
FHA (<i>B. pertussis</i>)	
	<i>17154501</i>
Pertactin (<i>B. pertussis</i>)	
	<i>33571840</i>
YadA (<i>Y. enterocolitica</i>)	
	<i>10955604</i>
	4324391
	28372996
	23630568
	32470319
SpaP (<i>S. mutans</i>)	
	<i>26007028</i>

	47267
PAC (S. mutans)	
	129552
SspA (Streptococcus gordonii)	
	25990270
	1100971
CshA (Streptococcus gordonii)	
	457707
CshB (Streptococcus gordonii)	
	18389220
ScaA (Streptococcus gordonii)	
	310633
SspB (Streptococcus gordonii)	
	25055226
	3220006
SpaA (Streptococcus sobrinus)	
	546643
PAG (Streptococcus sobrinus)	
	217036
	47561
Protein F (Streptococcus pyogenes)	
	19224134
PsaA (Streptococcus pneumoniae)	
	18252614
	7920456
	7920458
	7920460
	7920462
CbpA ^e / SpsA / PbcA/ PspC (Streptococcus pneumoniae)	
	14718654
	2425109

	2576331
	2576333
	3153898
	9845483
	19548141
FimA (Streptococcus parasanguis)	
	97883
SsaB (Streptococcus sanguis)	
	97882
EfaA (Enterococcus faecalis)	
	493017
FnbA (Staphylococcus aureus)	
	120457
FnbB (Staphylococcus aureus)	
	581562
	21205592
	13702452
BabA (Helicobacter pylori)	
	13309962
	13309964
	13309966
	13309968
	13309970
	13309972
	13309974
	13309976
	13309978
	13309980
	13309982
	13309984
	13309986
	13309988

13309990

13309992

13309994

Advantages:

1. The method helps in discovering putative adhesins, which are of great importance in drug discoveries and preventive therapeutics.
2. The method is useful in predicting the adhesive nature of even unique proteins,
5 because it is independent of the homology of the query proteins with other proteins.
3. This method is easy to use. For calculating the output, only the amino acid sequence is required as input. No other information is required to get the information about its adhesive nature.

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- 30

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Claims

1. A computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of:
 - a. computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, wherein the attributes are, (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition,
 - b. training a artificial neural Network (ANN) for each of the computed five attributes, and
 - c. identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51 .
2. A method as claimed in claim 1, wherein the protein sequences are obtained from pathogens, eukaryotes, and multicellular organisms.
3. A method as claimed in claim 1, wherein the protein sequences are obtained from the pathogens selected from a group of organisms comprising *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Mycoplasma pneumoniae*, *Mycobacterium tuberculosis*, *Rickettsiae prowazekii*, *Porphyromonas gingivalis*, *Shigella flexneri*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Neisseria meningitides*, *Streptococcus pyogenes*, *Treponema pallidum* and Severe Acute Respiratory Syndrome associated human coronavirus (SARS).
4. A method as claimed in claim 1, wherein the method is a non-homology method.
5. A method as claimed in claim 1, wherein the method uses 105 compositional properties of the sequences.
6. A method as claimed in claim 1, wherein the method shows sensitivity of at least 90%.
7. A method as claimed in claim 1, wherein the method shows specificity of 100%.
8. A method as claimed in claim 1, wherein the method helps identifies adhesins from distantly related organisms.
9. A method as claimed in claim 1, wherein the neural network has multi-layer feed forward topology, consisting of an input layer, one hidden layer, and an output layer.

10. A method as claimed in claim 9, wherein the number of neurons in the input layer are equal to the number of input data points for each attribute.
11. A method as claimed in claim 1, wherein the "P_{ad}" is a weighted linear sum of the probabilities from five computed attributes.
- 5 12. A method as claimed in claim 1, wherein each trained network assigns a probability value of being an adhesin for the protein sequence.
13. A computer system for performing the method of claim 1, said system comprising a central processing unit, executing SPAAN program, giving probabilities based on different attributes using Artificial Neural Network and in
10 built other programs of assessing attributes, all stored in a memory device accessed by CPU, a display on which the central processing unit displays the screens of the above mentioned programs in response to user inputs; and a user interface device.
14. A set of 274 annotated genes encoding adhesin and adhesin-like proteins,
15 having SEQ ID Nos. 385 to 658.
15. A set of 105 hypothetical genes encoding adhesin and adhesin-like proteins, having SEQ ID Nos. 659 to 763.
16. A set of 279 annotated adhesin and adhesin-like proteins of SEQ ID Nos. 1 to 279.
- 20 17. A set of 105 hypothetical adhesin and adhesin-like proteins of SEQ ID Nos. 280 to 384.
18. A fully connected multilayer feed forward Artificial Neural Network based on the computational method as claimed in claim 1, comprising of an input layer, a hidden layer and an output layer which are connected in the said sequence,
25 wherein each neuron is a binary digit number and is connected to each neuron of the subsequent layer for identifying adhesin or adhesin like proteins, wherein the program steps comprise:-
 - [a] feeding a protein sequence in FASTA format;
 - [b] processing the sequence obtained in step [a] through the 5 modules
30 named A, C, D, H and M, wherein attribute A represents an amino acid composition, attribute C represents a charge composition, attribute D represents a dipeptide composition of the 20 dipeptides [NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI

and HR], attribute H represents a hydrophobic composition and attribute M represents amino acid frequencies in multiplets to quantify 5 types of compositional attributes of the said protein sequence to obtain numerical input vectors respectively for each of the said attributes wherein the sum of numerical input vectors is 105;

[c] processing of the numerical input vectors obtained in step [b] by the input neuron layer to obtain signals, wherein the number of neurons is equal to the number of numerical input vectors for each attribute;

[d] processing of signals obtained from step [c] by the hidden layer to obtain synaptic weighted signals, wherein the optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually;

[e] delivering synaptic weighted signals obtained from step [d] to the output layer for assigning of a probability value for each protein sequence fed in step [a] as being an adhesin by each network module; and

[f] using the individual probabilities obtained from step [e] for computing the final probability of a protein sequence being an adhesin denoted by the P_{ad} value, which is a weighted average of the individual probabilities obtained from step [e] and the associated fraction of correlation which is a measure of the strength of the prediction.

19. A network as claimed in claim 18, wherein the input neuron layer consists of a total of 105 neurons corresponding to 105 compositional properties.

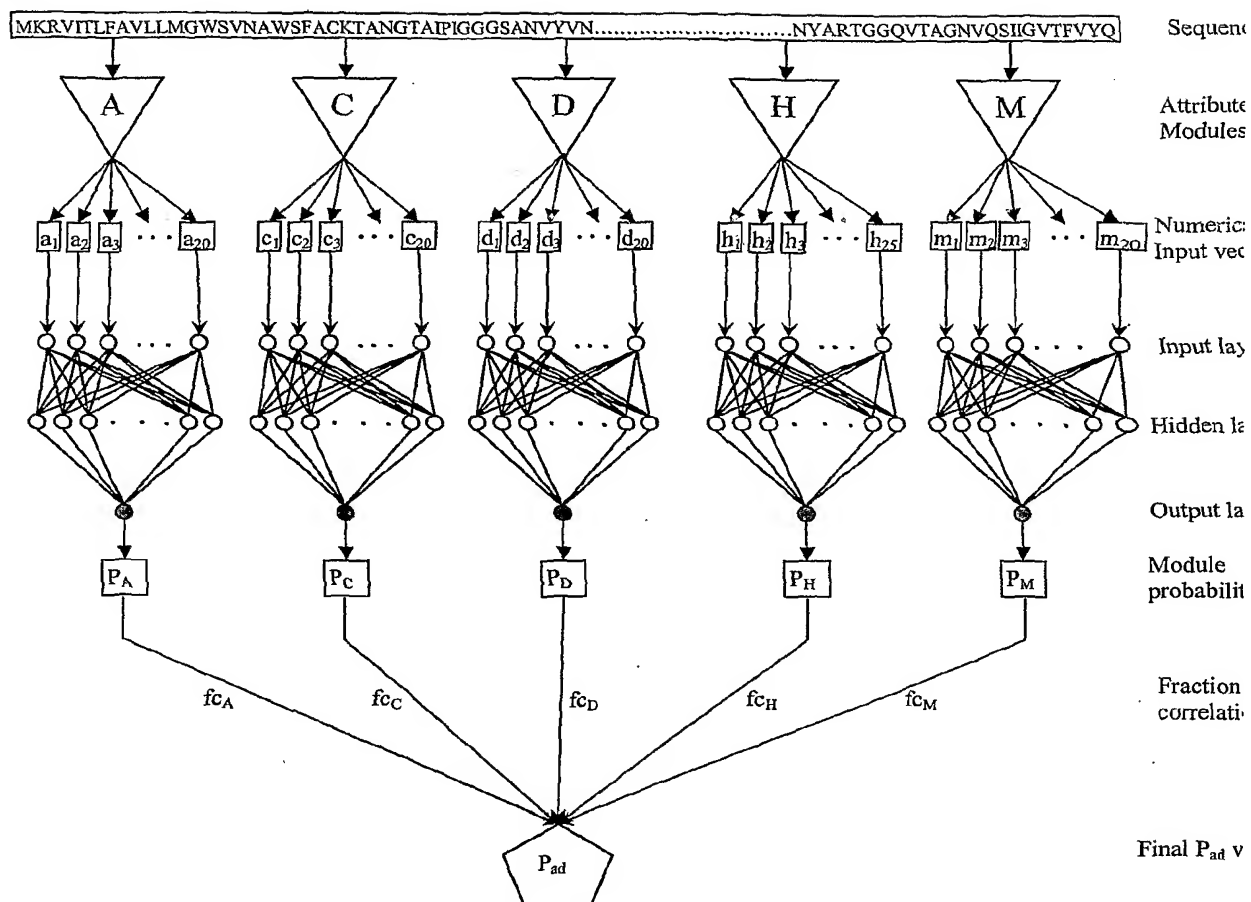
20. A network as claimed in claim 18, wherein the hidden layer comprises of neurons represented as 30 for amino acid frequencies, 28 for multiplet frequencies, 28 for dipeptide frequencies, 30 for charge composition and 30 for hydrophobic composition.

21. A network as claimed in claim 18, wherein the output layer comprises of neurons to deliver the output values as probability value for each protein sequence.

1/5

The Neural Network architecture

Figure 1



Assessment of SPAAN using defined test dataset.

Figure 2

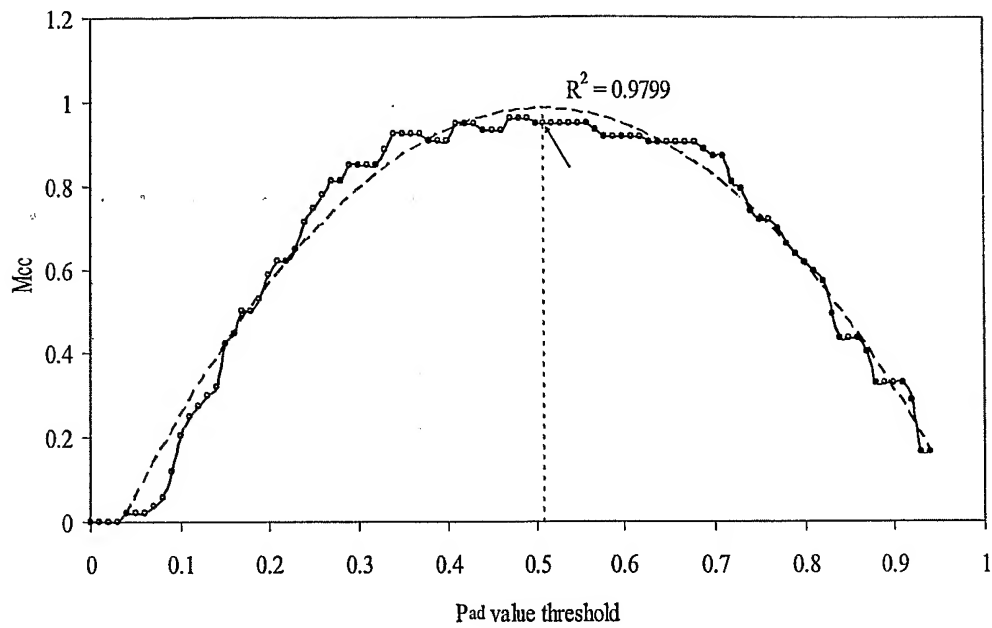


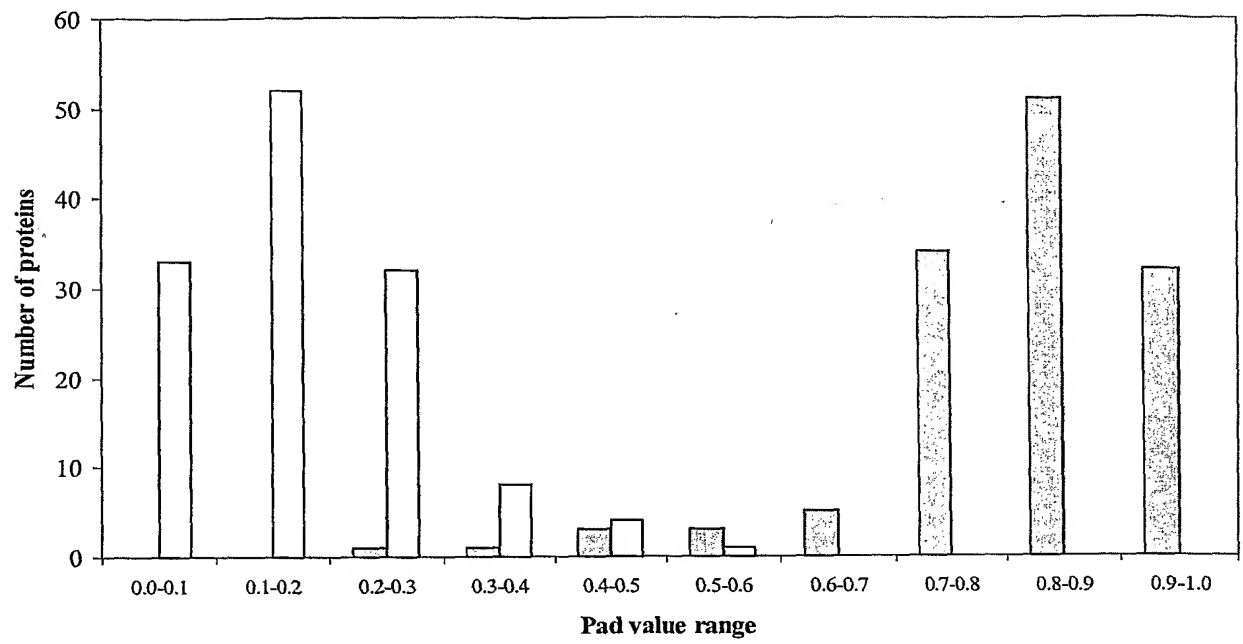
Figure 3 (a)

Figure 3 (b)

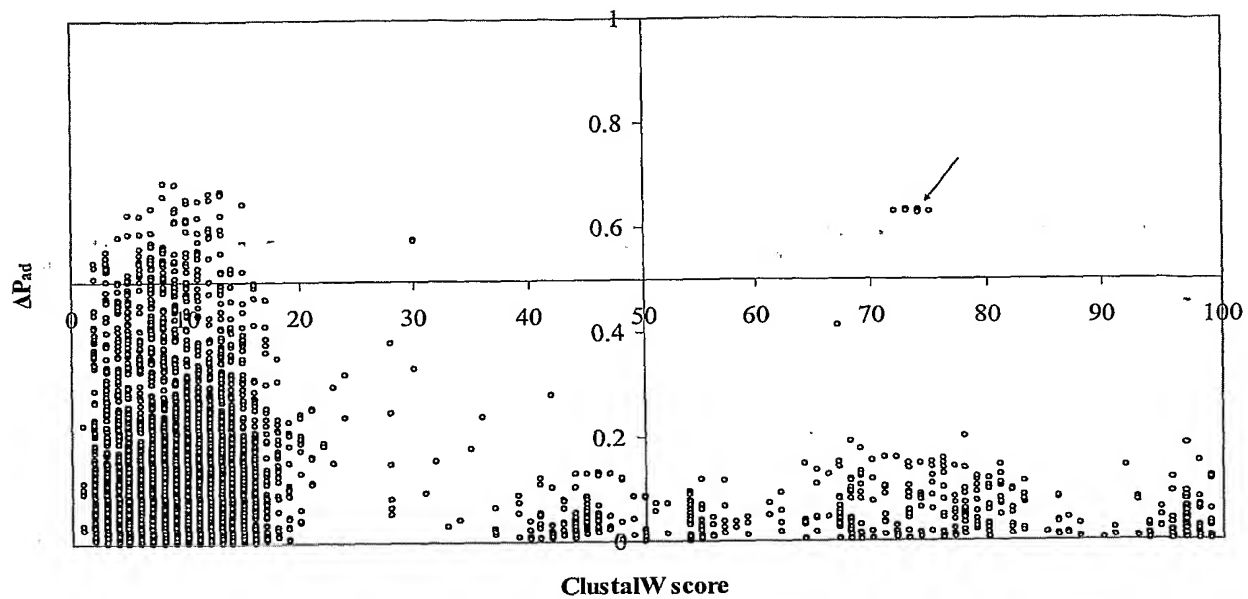
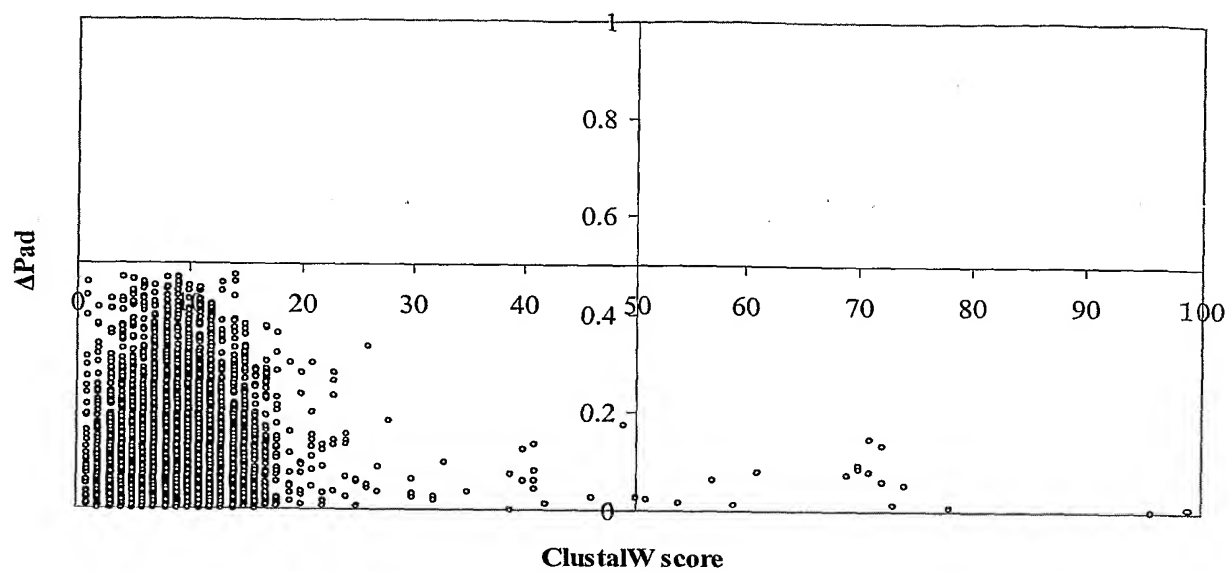


Figure 3(c)



Application Project

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MMFVLPKAR	LFIAFPKLT	VNTGGSLNTH	KLTLTTPPD	IQDDKLAGTS	VNGSTTLTST	120
LDNASPTEIL	SRNVVNGKV	SADELNVVAG	NNYVNAAGQV	TGSVSATGSR	NGYSVDVAKL	240
GGMYANKISL	VSTEKGVGVR	NLGVIAGGVN	GVSIDSKGNL	LNSNAQIQSA	STINLTNGT	300
LDNTTGTVTS	VGTLISLNTK	NTIVNTRAGN	ISTMGDIYVN	SGTIDNTNGK	LAAAGMLAVD	360
TNNATLINS	KGSSVGEIAG	LVALKTGTLN	NSNGQIRGGY	VGLESAALNN	NNGDIQTG	420
IAIISNGNVD	NNKGLIRSST	GHIVIGAAGS	VNNGSTKTAD	TGSSDSLGI	ADTGEVIGAN	480
NINNNGGQIA	SNGNVSLSSY	STIDDYAGKI	LSNSKVIIKG	SSLRNDTGGI	SGKQGEIVAV	540
GGSLTNNIGV	ISSEEGDISL	LANSVDNHGG	FMMGQNTIME	SMGCVNNNTA	LIVASKKLKI	600
NARGSLNIRD	GNFNGAYGL	YFGMPQQTGG	MVGKEGIELS	GQNIYNNNSR	LIAEDGPLTL	660
QAQNTFDNTR	ALVTSGADAS	IQVGGTYNN	YATTWSAGNL	DIDATTLQNS	SSGT MIDNNA	720
TGFIASDKNL	SLEVNSLTN	YGWISGKGDV	DVTVNNGNLY	NRNTIAAEKG	LDIAALNGIE	780
NWKDISAGGD	LTMTNHRHVT	NNSNSNMVGG	NIVINAVNDI	NNRGNIVSDA	DLNVTTKGNL	840
YNYLYMVGYG	DIALSANSVA	NNNATIEATG	DLIIDS KGNV	GNNRGNLHAL	NGVLSVKGN	900
LNNDNGEIRG	YGDVTLALTG	NYDSYKGSLT	SETGDVTLTA	NIVDNAYGLI	AGENVSVDAK	960
STIYNTALI	AANKKLIVINA	CGNLENRDGN	NFLRNNGALF	GITDNVGGIV	GKEGVTLTSAQ	1020
NYVNNSSII	AENGPLNLLS	RGTLDNTRAL	LSSGADAIIR	AAGTFYNNYA	TTYSAGNLDV	1080
YAASLNNASD	GRLEDNTATG	VIASDKNLDL	SVDNSVTNYG	WISGKGDVHF	NVLKGTLYNR	1140
NAIAADNALT	INALNGVENF	KDIVAGTALT	IDTQKYVTNN	SNSNMLGQTI	AINAVNDIMN	1200
RGNIVGDYSL	GVKTTGNIYN	YLNMLSYGVA	GVSANKVTNS	GKDAVLGGFY	GLALEANETD	1260
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Sequence

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LIESGGYQDV	GRHNNYVQGS	NNTTINGGRQ	SIHDGGISTG	TIESGNQDV	YKGGISNGTT	180
IKGGASRVEG	GSANGTLIDG	GSQIVKVQGH	ADGTINKSG	SQDVVQGSIA	TNTTINGGRQ	240
YVEQSTVETT	TIKNGGEQRV	YESRALDTTI	EGGTQSLNSK	STAKNTQIYS	GGTQIIDNTS	300
SSDVIEVYSG	GVLVDVSGGTA	TNVTQHDGAI	LKNTNTNGTTV	SGTNSEGAFS	IHNHVADNVL	360
LENGGHLIDIN	AYGSANKTII	KDKGTMSVLT	NAKADATRID	NGGVMDVAGN	ATNTIINGGT	420
QNIINNYGIAT	GTNINSGTQN	IKSGGKADTT	IISSGSRQVV	EKDGTAIGSN	ISAGGSLIVY	480
TGGIAHGVNQ	ETGSALVANT	GAGTDIEGYN	KLSHFTITGG	EANYVVLENT	GELTVVAKTS	540
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EGTNSYGDFA	YIRNSEAKNV	VLENAGSLTV	VTGSRAVDTI	INANGKMDVY	GKDVGTVLNS	660
AGTQTIYASA	TSDKANIKGG	KQTVYGLATE	ANIESGEQIV	DGGSTEKTHI	NGGTQTVQNY	720
GKAINTDIVS	GLQQIMANGT	AEGSIINGGS	QIVNEGLAE	NSVLNDGGTL	DVREKGSATG	780
IQQSSQGALV	ATTRATRVTG	TRADGVAFSI	EQGAANNILL	ANGGVLTVES	DTSSDKTQVN	840
TGGREIVKTK	ATATGTTLTG	GEQIVEGVAN	ETTINDGGIQ	TVSANGEAIK	TTINEGGTIL	900
VNDNGKATDI	VQNSGAALQT	STANGIEISG	THQYGTFSIS	GNLATNMLLE	NGGNLLVLAG	960
TEARDSTVGK	GGAMQNQGQD	SATKVNSSGGQ	YTLGRSKDEF	QALARAEDLQ	VAGGTAIVYA	1020
GTLDASVSG	ATGSLSLMTP	RDNVTPVKLE	GAIRITDSAT	LTIGNGVDTT	LADLTAASRG	1080
SVWLNSNNSC	AGTSNCEYRV	NSLLLNDGNV	YLSAQTAAPA	TTNGIYNTLT	TNELSGSGNF	1140
YLHTNVAGSR	GDQLVVNNNA	TGNFKIFVQD	TGVSFQSDDA	MTLVKTGGGD	ASFSLGNTGG	1200
FVDLGTIEYV	LKSDGNSNWN	LTNDVKPNPD	PNPNNPNPK	PDPKPDPKPD	PKPDPPTPEPT	1260
PTVPPEKRIT	PSTAAVLNMA	ATLPLVFDAE	LNSIRERLNI	MKASPHNNNV	WGATYNTRNN	1320
VTTDAGAGFE	QTLTGMTVGI	DSFNDIPEGI	ATLGAFMGYS	HSHTGFDRGG	HGSVGSYSLG	1380
GYASVHESEG	FYLDGVVKLN	RFESNVAGKM	SSGGAANGSY	HSNGLGGHIE	TGMRFTDGN	1440
NLTPYASLTG	FTADNPYHL	SNGMESKSD	TRSIYRELGA	TLSYNMRLGN	GMEIEPWLKA	1500

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AQNTAAYYKS ACPACTTARF AATHATDAAL SAPALNTSAG QAASSAQAS SSAGTASTKA 150
15 TEASKSAAAA ESSKSAAATS AGAAKTSETN AAVSQQSAAT SASTATTKAS EAASSARDAS 240
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AAGSATAAAQ SKSTAESAAT RAETAACKRAE DIASVALED ASTTKKGIVQ LSSATNSTSE 480
20 SLAATPKAVK AAYELANGKY TAQDATTAQK GIVQLSNATN STSEMLAATP KSVKAAAYDLA 540
NGKYTAQDAT TAQKGIVQLS SATNSASETL AATPKAVKAA NDNANGRVPS ARKVNGKALS 600
SDITLTPKDI GTLNSTTMSF SGGAGWFKLA TVTMPQASSV VSITLIGGAG FNVGSPQQAG 660
ISELVLRAGN GNPKGITGAL WQRTSTGFTN FAWVNTSGDT YDIYVAIGNY ATGVNIQWDY 720
TSNASVTIHT SPAYSANKPE GLTDGTVYSL YTPSEQFYPP GAPIPWPSDT VPSGYALMQG 780
25 QTFDKSAYPK LAAAYPSGVI PDMRGWTIKG KPASGRAVLS QEQDGIKSHS HSASASSTDL 840
GKTKTSSFDY GTKSTNNTGA HTHSVSGTAA SAGNHHSVT GASAVSQWSQ NGSVHKVUSA 900
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40 DKPWPVALYL TPVSSAGGVA IKAGSLIAVL ILRQTKNYSN DDFQFVWNIY ANNDVVVPTG 180
GCDVSARDVT VTLPDYPGSV PIPLTVYCAK SQNLGYLBSG TTADAGNSIF TNTASFSPAQ 240
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55 VGIGIETAGG AAVPINSTTG ASFPLNQGN SVNFNAWLQT VNGRNVTSKD FTATMTVTFE 180
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GGLATGTIIN TGAEGGPDSD NSYTGQKVQG TAESTTINKN GRQIILFSGL ARDTLIYAGG 240
DQSVHGRALN TTLNGGYQYV HRDGLALNTV INEGGWQVVK AGGAAGNTTI NQNGELRVHA 300
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5 TLVDDGGLA VSAGGKATSV TITSGGALIA DSGATVEGTN ASGKFSIDGT SGQASGLLLE 420
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EIRFDNQTP NAALSRVAK SNSPVTFHL TTTNLTGQGG TINMRVRLDG SNASDQLVIN 540
GGQATGKTWL AFTNVGNSNL GVATTGQGR VVDAQNGATT EEGAFALSRP LQAGAFNYTL 600
NRDSDEWYL RSENAYRAEV PLYTSMLTQA MDYDRILAGS RSHQTGVNGE NNSVRLSIQG 660
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DGSRAGTVRD DAGSLGGYLN LVHTSSGLWA DIVAQGRHS MKASSDNDF RARGWGLGS 780
LETGLPFSIT DNLMLPQLQ YTWQGLSLDD GQDNAGYVKF GHGSAQHVRA GFRLGSHNDM 840
TFEGTSSRD TLRDSAKHSV SELPVNWWVQ PSVIRTFSSR GDMSMGTA AAA GSNMTFSPSR 900
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ISVLNAGYTA VPFEHVSNOA TTTDHTCQGN KTTAVGVSLK TGADAKISFR IKRSINGTVV 180
IPITDIALLY ANISSTTTTG EAIKVRISG SLTAPQSCQI NAGQVIYFDF DTIPASEFSS 240
TAGQAITSRK ITKTVSIET GMGYERTQKV DASFTGTNRS SDDTMVATDN ADVGIKIYNK 300
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KLNVDKDFSL KDSSLEMLYP IYDTPTNMLF TQGAHRTDD RTQSNIGFGW RHFGSGNDWMA 180
GVNFTFIDHDL SRSHTRIGVG AEYWRDYLKL SANGYIRASG WKKSPDIEDY QERPANGWDI 240
RAEGYLPAPW QLGASLMEYQ YYGDEVGLFG KDKRQKDPHA ISAEVTTYTPV PLLTSLAGHK 300
45 QKSGGENDTR FGLEVNRYRIG EPLAKQLDTE SIRERRVLG SRYDLVERN NIVLEYRKSE 360
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RAFSEQYQLG TLQOTLKFFVA GPLDAAHSSI TLNPDKPVVG GTVTAIWTVK DAYDNPVTS 720
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TVVDTYGNPL QGQEVTLTL VQVTSKTGNT VTTNAAGKAD IELMSTVAGE HNISASVNGA 1080
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GVKPLTGDNV WVKANDEGKA ELQVVSVTAG TYEITASAGN SQPSNTQTIT FVADKATATV 1200
60 SGIEVIGNYA LADGNAKQTY KVTVTDANN LLDKSEVTLT ASPANLVLT NGTAKTNEQG 1260
QAIFTATTTV AAKYTLTAKV SQADQGESIS TAESKFVADD TNAVLTASSD VTSLVADGIS 1320
TAKLEVTLMS ANNPVGGNMW VDIKTPEGVT EKDYQFLPSK NDHFVSGKIT RTFSTSKPGV 1380
YTFTFNALTY GGYEMKPVTV TITAVDADTA KGEEAMN 1417
65 <212> Type : PRT
<211> Length : 1417
SequenceName : SEQ ID 8
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
5 MARGWASSEA SGAMTDWLNN FGTARISLGV DEDFSLKNSQ FDFLHPWYDT PDYLLESQHT 60
LHRTDDRTQI NTGLGWRHFT SSWMSGINLF FDHDLTRYHS RAGLGAEYWR DYLLKSSNAY 120
IGLTGWRSAE ELDNDFEARP ANGWDLRAEG WLPAPWQLGG KLVYEQYYGD EVALFDKNDR 180
QSNPHAITAG LNYTPFPPLLT LSAEQRQKQ GENDTRFAVD LTWQPSSSMQ KQLNPDEVAG 240
10 RRSLAGSRYD LIDRNNNIVL EYRKKELRRL SLDDPVKGKS GEIKPLVSSL QTKYALKGYN 300
IEAAALEAAG GKVSTSGKDI TVTLPGYRFT NTPETDNTWS IDVTAEDVKG NLSRHEQSMV 360
VIQAPTLQSK DSSLNVNPLT VAADKKSTTT LTVTAHDSGD TPVPGLALQT RSEGVQDITL 420
SDWTNNGDGS YTOILTATTT SGSVTLTPQI NGESAVKESI VVNIVPVVSS RDHSSITIDN 480
VSYVAGNDIK VRVELKDDSN QFVAYQKEEL VKAVTVENSK PGATIVWHEE QPGVYAANYF 540
15 AYKQGTALRA QLSLHNWNP LQSHIYNIEA NQNKARVATL SATNNDVYAD KKTFTNLTIN 600
VTDESDNPLT NHQVTFKNEK GSAEFVEPPQ QNTDAYGVAT INMVSQVAEE NTISATLPNG 660
FSQRIIAKFV SDSSTPKFKQ LVADPDITIA GNSQGSTLTA IITDFHNNPL KDMKVNFPVAP 720
GGSQDLNNTTA TTDQSGIVRV HLTSSKAGSY SVDASLEVDK NIHQSVTITV VPNREQSVMT 780
LNAGSGSAIA NNTNIVTLTA SVKDVYGHPL PDEDVKFTLP ASMTGNFTLS SETARTDANG 840
20 DAVVTLRGTK AGEFTVTATL TRNNTVAYQQ VTFIGDNTSA QLQPLTASLN SIVAGNSTGS 900
TLTATILDAY QNPLKQDLVT PQSNDVTLSE TEVTNTLTGQ ATVTMTSNIA GQHNVVVSRK 960
AQASDNDIKF VSVLDESSA KVISITGAEK TITVGENITL RILVQDAFNN VIAGQVRRLS 1020
AQPTTNITIG DTAYTDNNGY AYVNLSTQP GVVQVTATLD NNSSSKVDVN VANGKLELTS 1080
SKPETTVHNS EGITLTATAR NARGELMPGQ IITFSVTPEG ATLSNTGEVL TDQSGQAKVT 1140
25 LTSDKVNVTY VTAIMGKDVV VQSQVTVAVK ADAKTAHVVS VVASPDITTA DGIDSSTITS 1200
RVEDDYGFPV RSVLDISHGLD TKGSPVNVIP TITRTDQSGQV TATITSTLAE TLTNVQVPG 1260
TANQSATITL VAGTADESKS ILKSDVDTLK ADYQQSAKLT LTLQDKYGNP IVTSDHLEFV 1320
QSGPFVNFLEK LSDIDYSQRN YGEYTVTVTG GKEGTATLIP MLNGVHQANL SISLNLIQSI 1380
KEMSGHVIAN NHTFSTAKFP SEGFAAYYT LNNDNFEAGK TVDDYMFSSS QGWVSVDSAG 1440
30 KVSFANIGDQ TSVTISAVPR QGGTTYQTLI KLGKWWVWNG NHTNIWLAAN ALCHAKNDGY 1500
NLPGITHLTS GENKRTQGS L YGEWGNVGAF SSNSQFTPGA YWTSESDDYS RHYYVQMLTG 1560
MTGSDADSSP QLTACRKS L 1579
<212> Type : PRT
<211> Length : 1579
35 SequenceName : SEQ ID 9
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
40 MITHGCYTRT RHKHKLLKKT L IMLSAGLGLF FYVNQNSFAN GENYFKLGSD SKLLTHDSYQ 60
NRLFYTLKTG ETVADLSKSQ DINLSTIWSL NKHLYSSESE MMKAAPGQOI ILPLKKLPFE 120
YSALPLLGS A PLVAAGGVAG HTNKLTKMSP DVTKSNTDD KALNYAAQQA ASLGSQQLSR 180
45 SLNGDYAKDT ALGIAGNQAS SQLQAWLQHY GTAENVLQSG NNFDGSSLDL LLPFYDSEKM 240
LAFGQVGARY IDSRFTANLG AGQRFFLPAN MLGYNVFIDQ DFGSDNTRLG IGGEYWRDYF 300
KSSVNGYFRM SGWHESYNKK DYDERPANGF DIRFNGYLP YPALGAKLIY EQYYGDNVAL 360
FNSDKLQSNP GAATVG VNYT PIPLVTMGID YRHGTGNEND LLYSMQFRYQ FDKSWSQQIE 420
PQYVNELR TL SGRYDLVQR NMNIILEYKK QDILSLNIPH DINGTEHSTQ KIQLIVKSKY 480
50 GLDRIVWDDS ALRSQGGQIQ HSGSQSAQDY QAILPAYVQG GSNIYKVTAR AYDRNGNSSN 540
NVQLTITVLS NGQVVDQGVG TDFTADKTS A KADNADTITY TATVKKNGVA QANVPVSFNI 600
VSGTATLGAN SAKTDANGKA TVTLKSSTPG QVVVSATAE MTSALNASAV IFFDQTKASI 660
TEIKADKTTA VANGKDAIKY TVKVMKNGQP VNNQSVTFST NFGMFNGKSQ TQATTGNDGR 720
ATITLTSSSA GKATVSATVS DGAEVKATEV TFFDELKIDN KVDIIGNNVR GELPNIWLYQY 780
55 GQFKLKASGG DGTYSWYSEN TSIATVDASG KVTLNGKGSV VIKATSGDKQ TVSYTIKAPS 840
YMIKVDKQAY YADAMSICKN LLPSTQTVLS DIYDSWGAAN KYSHYSSMNS ITAWIKQTSS 900
EQRSGVSSTY NLITQNPLPG VNVNTPNVYA VCVE 934
<212> Type : PRT
<211> Length : 934
60 SequenceName : SEQ ID 10
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
65 MLVLSESFKN KLLPMNGYMK GGSDSGSKAQ ARATEKGIEL QREMWQTNMQ NLAPFTPLAQ 60

QYVSQQLQNL SLOGGQQAALN QYYSQQYKD LAGQARYQSL AAAEATGGLG STATGNQLAA 120
IAPTILGQNL SGQMNNYNNL ANIGLGALTG QANAGQNYAN NVSQLYQQQA AASAANANKP 180
SGLQSFATGA IGGAASGAMI GSAVPVIGTG IGALAGGVIG GLGSLF 226
<212> Type : PRT
5 <211> Length : 226
SequenceName : SEQ ID 11
SequenceDescription :

Sequence

10 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKILSGLIL LLCCPYGFAA NGDGATHMSN LSFGLPTVAA ANNHSGYNIF EALSNTTGTY 60
PVRCHCDDTH GGPGQQTAF FIFYTGDAAP GLVLERTLNG LNYALNDYL SVGVTFIFIIN 120
15 NQYAAIPFEH LSNQSTSPQH TCGAGNNGST VNLDSGRSAK LSFYVRHSIT GTVTIPTTEV 180
AWLYAGMSDH FPKTTPVSKV TIRGQLTAPQ NCELTPNQSI DVDFQKINSA EFSSTAGSII 240
AERKIKTEVT VSCGTMEDVR STEVVSASMI AANRSADATM IVTSNPDVGI KIPDKNDRPV 300
NVDGGNLPAD MGAISRLGKT DGSVTFYSAP ASLTGAKPAP DNGFTATATL VIEFTN 356

20 <212> Type : PRT
<211> Length : 356
SequenceName : SEQ ID 12
SequenceDescription :

Sequence

25 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNKIYRLKWN RSRNCWSVCS ELGSRVKGKK SRAVLISAIS LYSSLVFADD VIVNQDKTID 60
30 FGKENQSDY RITVTDNANL VINATDTSRP RLTLASGGGL DITGGKVTIN GPLNFLKGT 120
GFLNVSNAGS ELYADDLYES NSGMRHDRGY FNVSNGGKIH VKGTSRLTYL QGNVSGEGSQ 180
VNSETFFMGV YGSYGGNQYL SVNNGGEVNA RKQISLGYYD QVSDTTLAVS EGGKISAPTI 240
SLSTNSLAL GAQEGSAKA AGIIDAIEKIE FVWAKTSEKK ITLNHTDKDA TISADIVSGS 300
EGLGYINALN GTTYLTGDNS AFSGKVKIEQ NGALGITQNI GTAEINNRGK LHLKADDSMT 360
35 FANKISNGT ISIDSGTVEL TGNNAFSGY IDVASGAVAV ISEDKNIGRA ELDVDGKLQI 420
NANKDWFDN DLEGRGIVEI NMGNHEFSFD EFAYTDWFQ SLAFQNTTFN LEKNAEFLQK 480
GGITAGQSSL VTVGKAHSI STLGFSGGTV DFGALTAGAQ MTEGTVNVSK TDLRGEVVI 540
QVSDSDVVRV VSRDIDSALS LTEVDDGNS IKLVDAGAE VLGDAGNLQL QDKNGQILSS 600
SAQRDIQNG QKAAVGTYDY RLTSQVNNND LYIGYGLTQL DLHATDS DAL VLSSNGKSEN 660
40 AADLSAKITG SGDLAFSSQK GQTVSLSNKD NDYTGVTDLR SGTLLLNNDN VLGNTHLRL 720
AAETELDMNG HSQTVGTLNG SADSLSLNG GSLTVTNGGT STGSLTGSGE LNIQGGTLDI 780
AGDNSNL TAN VNIAANSANVL VSHAQGLGSA NVENNGTLAL NNSAEKRAAA SVNYALGGNL 840
TNNGTLMTGM SGQQAGNVLV VKGNYHGNG QLVMTVNLG DDSVTDKLVV EGDTS GTTAV 900
TVNNAGTGGA KTLNGIELIH VDCKSEGEFV QAGRIVAGAY DYTTLARGQGA NSGNWYLTSG 960
45 SDSPELQPEP DPMNPPEPNP NPEPNPNPTP TPGPDLNVND DLRPEAGSYI ANLAAANTMF 1020
TTRLHERLGN TTYTDMVTGE QKQTTMWMRH EGGHNKWRDG SGQLKTQSNR YVLQLGGDVA 1080
QWSQNGSDRW HVGVMAGYGN SDSKTISSRT GYRAKASVNG YSTGLYATWY ADDES RNGAY 1140
LDSWAQYSWF DNTVKGDDLQ SESYKSKGFT ASLEAGYKHK LAEFNGSQGT RNEWYVQPQA 1200
QVTWMGVKAD KHRESNGTLV HSNGDGNVQT RLGVKTVLKS HHKMDGKSR EFQPFVEVNW 1260
50 LHNSKDFSTS MDGVSVTQDG ARNIAEIKTG VEGQLNANLN VWGNVGVQVA DRGYNDTSAM 1320
VGIKWQF 1327
<212> Type : PRT
<211> Length : 1327
SequenceName : SEQ ID 13
55 SequenceDescription :

Sequence

60 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MITMKKSVLT AFITVVCATS SVMAADDNAI TDGSVTFNGK VIAPACTLVA ATKDSVVTLP 60
DVSATKLQTN GQVSGVQTDV PIELKDCDTT VTKNATFTN GTADTTQITA FANQASSDAA 120
TNVALQMYMN DGTTAIKPDT ETGNILLQDG DQTLTFKVDY IATGKATSGN VNAVTFNHIN 180
YY 182
65 <212> Type : PRT
<211> Length : 182
SequenceName : SEQ ID 14

SequenceDescription :

Sequence

5 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSKFVKTAIA ATMVMGAFAS TSTIAAGNNG TARFYGTIED SPCSIVPDDH KLEVDMGDIG 60
SGILKNNGTS TPKAFQIHLQ DCVFDTQTTM TTTFTGNASS TNSGNYITY NTDTGAFFNN 120
VSLAIGDAQG TSYKSGAGIE QKIVNDTATN KGKAKQTLDF KAWLVGAADA PDLGNFEANT 180
10 TFQITYL 187
<212> Type : PRT
<211> Length : 187
SequenceName : SEQ ID 15
SequenceDescription :

15

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
20 MRVIFLRKEY LSLLPSPMIAS LFSANGVAAA IDLCQGYDIK ASCHASRQSL SGITQVWSIA 60
DGQWLVSFDM TNNASGGAVF LQQGAFTLS PENETGMTLF ANNTVSGEYN NGGAI FAKEN 120
STLNLTDVIF SGNVAGGYGG AIYSSGTNDT GAIDLRTVNA VFRNNIANDG KGGAIYTINN 180
DIYLSDDVFN NNQAYTSTSY SDGDGGAI DV TDNNSDSKHP SGYTIINNTA FTNNTAEGYG 240
GAIYTN SATA PYLIDISVDD SYSQNGGVLV DENNSAAGYG DGPSSAAGGF MYLGLSEVTF 300
25 DIADGKTLVI GNTENDGA VD SIAGTGLITK TSGSDLVLNA DNNDFTGEMQ IENG EVTLGR 360
SNSLMNVGDT HCQDDPQDCY GLTIGSIDKY QNQAELNVGS TQQTFAHSLT GFQNGTLNID 420
AGGNVTVNQG SFAGTTEGAG QLTIAQNGSY VLAGAQSMAL TGDIVVDAGA VLSLEGAAD 480
LAALQDDPQS IVLNGGMLDL SDFSTWQSGT SYKDGLEVSQ SSGTVIGSQD VVDLAGGNM 540
HIGGDGKDGW YVVIDAGDGQ VSLANDNQYL GTTQIASGTL MVSDNSQLGY THYNRQVIFT 600
30 DKPQESVMEI TANVDTRSTT TEHGRDIEMR ADGEVAVDAG VDTQWGALMA DSSGQHDEG 660
STLTKTGAGT LELTAGSTTQ SAVRVEEGLT QGVADIFPY ASSLWVGDA TFFTADQDI 720
QSIDATSSGT IDISDGTFLR LTGQDTSVAL NASLFNC DGT LVNATDGVTL TGE LNTNLET 780
DSLTYLSNVT VNGNLNTSG AVSLQNGVAG DTLTVNGDYT GGGLLLDSE LNGDSDVSDQ 840
LVMNGNTAGN TTVVNSITG IGEPTSTGIK VVDFAADPTQ FQNNAQFSLA GSGYVNMGAY 900
35 DYTLVEDNND WYLRSEQVTP PSPDPDPTP DPDPDPTP TPDPEPTPAY QPVLNAKVGG 960
YLNLRANQ AFMMERRDHA GGDGQTLNLR VIGGDYHYTA AGQLAQHEDT STVQLSGDLF 1020
SGRWGTDGEW MLGIVGGYSD NQGDSSRSMT GTRADNQNHG YAVGLTSSWF QHGKQKQAW 1080
LDNWLQYAWF SNDVSEHEDG VDHYHSSGII ASLEAGYQWL PGRGVVIEPQ AQVIYQGVQQ 1140
DDFTAANRAR VSQSQDDIQ TRLGLHSEWR TAVHVIPTLD LNYHDPHST EIEEDASTIS 1200
40 DDAVKQRGEI KVGVTGNISQ RVSLRGSVAW QKGSDDFAQT AGFLSMTVKW 1250
<212> Type : PRT
<211> Length : 1250
SequenceName : SEQ ID 16
SequenceDescription :

45

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
50 MHSWKKKLIV SQLALACTLA ITSQANAATN DISQTYNTF HHYN DATYAD DVYYDGYVGW 60
NNYAADSYN GDIYPVINNA TVNGVISTYY LDDGISTNTN ANSLTIKNT IHGMITSECM 120
TTDCADDRAT GYVYDRLTSL VDNSTIDDNY EHYTYNGTYN NAADTHVVDV YDMGTAITLD 180
QEV DLSITNN SHVAGITLTQ GYEWEDIDDN TVSTGVNSSE VFNNTITVKD STVTSGSWTD 240
EGTTGWFGHT GNASYSNTL TADDVAIAAI ANPYADNAMQ TTVTLDNSTL MGDVVFSSNF 300
55 DENFFPQGAN SYRDADGDVD TNGWDGTD RM DVTLNNGSKW VGAAMSVHMV DEDGDGSYDG 360
YAVGTEATAT LLDIAANSLW PSSTVGVDNI NTQYDENGHI VGNEVYQSGL FNVTLNGGSE 420
WDTTKSSLID TLSINSGSQV NVADSRLLSD TVSLTGGSNL NIGEDGHVAT NTLTIDNSTV 480
KMSDDVSAGW GLEDAALYAN TITVTNDGLL DINVDQFDAN PFQADTLNLT STTD TNGNIH 540
AGVFDIHSSD YVMDTDLVND RTNDTTSKNY GYGLIAMNSD GHLTINGNGD NDNTASIEAG 600
60 QNEVDNNGDH VAAATGNYKV RIDNATGAGS IADYNGNELI YVNDKNSNAT FSAANKADLG 660
AYTYQAEQRG NTVVLQOMEL TDYANMALSI PSANTNIWNL EQDVTGTRLT NSRHGLADNG 720
GAWVS YFGGN FNGDNGTINY DQDVNGIMVG VDTKIDGNA KWIVGAAAGF AKGDMNDRSG 780
QVDQDSQTAY IYSSAHFANN VFVDGSLSYS HPMNDLSATM SNGTYVDGST NSDAWGFLK 840
AGYDFKLGA GYVTPYGSIS GLFQSGDDYQ LSNMVKVDGQ SYDSMRYELG VDAGYFTTYS 900
65 EDQALTPYFK LAYVVDSDNN DNDVNGDSID NGTEGSAVRV GLGTQFSFTK NFSAYTDANY 960
LGGGDVDQDW SANVGKYTW 980
<212> Type : PRT

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<211> Length : 980
      SequenceName : SEQ ID 17
      SequenceDescription :

5  Sequence
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   <213> OrganismName : Escherichia coli O157:H7
   <400> PreSequenceString :
10  MKLLKHVGMIV VSVLAMSSAA VSAAEGDESV TTTVNGGVIH FKGEVVNAAC AIDSESMNQT      60
   VELGQVRSSR LAKAGDLSSA VGFNIKLNDC DTNVSSNAAV AFLGTTVTSN DDTLALQSSA      120
   AGSAQNVGIQ ILDRITGEVLI LDGATFSAKT DLIDGTNILP FQARYIALGQ SVAGTANADA      180
   TFKVQYL                                          187
   <212> Type : PRT
   <211> Length : 187
15  SequenceName : SEQ ID 18
   SequenceDescription :

   Sequence
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20  <213> OrganismName : Escherichia coli O157:H7
   <400> PreSequenceString :
   MKLLKVAATA AIVFSGSALA GVVFPQYGGGG GNGHGGGNNS GPNSSELNIYQ YGGGNSALAL      60
   QADARNSDLT ITQHGGGNGA DVGQGSDDSS IDLTQRGFGN SATLDQWNGK DSHMTVKQFG      120
   GGNGAAVDQT ASNSTVNVITQ VGFGNNATAH QY                                          152
25  <212> Type : PRT
   <211> Length : 152
   SequenceName : SEQ ID 19
   SequenceDescription :

30  Sequence
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   <213> OrganismName : Escherichia coli O157:H7
   <400> PreSequenceString :
35  MPIGNLGHNH NVNNSIPPAP PLPSQTDGAG GRGQLINSTG PLGSRALFTP VRNSMADSGD      60
   NRASDVPLP VNPMLAASE ITLNDGFEVL HDHGPLDTLN RQIGSSVFRV ETQEDGKHIA      120
   VQQRNGVETS VVLSDQYAR LQSIDPEGKD KFLVTGGRGG AGHAMVTVAS DITEARQRIL      180
   ELLEPKGTGE SKGAGESKGV GELRESNSGA ENTETQTST STSSLRSDPK LWLALGTVAT      240
   GLIGLAATGI VQALALTPEP DSPTTDPDA AASATETATR DQLTKEAFQN PDNQKVNIDE      300
   LGNAIPSGVL KDDVVANIEE QAKAAGEEAK QQAIENNAQA QKKYDEQQAK RQEELKVSSG      360
40  AGYGLSGALI LGGGIGVAVT AALHRKNQPV EQTTTTTTTT TTTSARTVEN KPANNTPAQQ      420
   NVDTPGSEDT MESRRSSMAS TSSTFFDTSS IGTVQNPYAD VKTSLHDSQV PTSNSNTSVQ      480
   NMGNTDSVYV STIQHPPRDT TDNGARLLGN PSAGIQSTYA RLALSGGLRH DMGGLTGGSN      540
   SAVNTSNNPP APGSHRFV                                          558
   <212> Type : PRT
45  <211> Length : 558
   SequenceName : SEQ ID 20
   SequenceDescription :

   Sequence
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50  <213> OrganismName : Escherichia coli O157:H7
   <400> PreSequenceString :
   MFSTFKKAAL LAAIALPFST MAAPTIVTFQG EVTDTQTCVN INGQINSVVL MPTVAMADFG      60
   ATLLADGQSAG QTPFTVSVSN CQAPTQADQA INTTFLGYDV DASTGVMGMR DTSSDAAKGF      120
55  GIQLMDSSTS GNPVTLAGAT NVPGLTLKVG DTEASYDFGA RYFVIDSAAA TAGKITAVAE      180
   YTLSYL                                          186
   <212> Type : PRT
   <211> Length : 186
   SequenceName : SEQ ID 21
60  SequenceDescription :

   Sequence
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   <213> OrganismName : Escherichia coli O157:H7
65  <400> PreSequenceString :
   MNSEGKPGN VLTVNGNYTG NNGLMTFNAT LGGDNSTPK MNVKGDTQGN TRVRVDNIGG      60
   VGAQTVNGIE LIEVGNSAG NFALTGTGVE AGAYVYTLAK GKGNDKKNWY LTSKWDGVTP      120
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ADTPDPINNP PVVDPEGPSV YRPEAGSYIS NIAAANSIFS HRLHDLGEP QYTDSLHSQD 180
SASSMWMRHV GGHERRSSAGD GQLNTQANRY VLQLGGDLAQ⁺ WSSNAQDRWH LGVMAGYANQ 240
HSNTQSNRVG YKSDGRISGY SAGLYATWYQ NDANKTGAYV DSWALYNWFD NSVSSDNRSA 300
DDYDSRGVTA SVEGGYTFFEA GTCSGSEGTL NTWYVQPQAQ ITWMGVKDSH HARKDGTRE 360
5 TEGDGNVQTR LGVKTYLNSH HQRDDGKQRE FQPYIEANWI NNSKVYAVKM NGQTVSRDGA 420
RNLGEVRTGV EAKVNNNLSL WGNVGVQLGD KGYSDTQGM L GVKYSW 466
<212> Type : PRT
<211> Length : 466
SequenceName : SEQ ID 22
10 SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
15 <400> PreSequenceString :
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VADLSRFENG QELPPGTYRV DIYLNNGYMA TRDVTFTNGD SEQGIVPCLT RAQLASMGLN 120
TASVAGMNL ADDACVPLTT MVQDATAHLD VGQQRNLNLT PQAQFMSNRAR GYIPPELWDP 180
GINAGLLNLYN FSGNSVQNRI GGNSHYAYLN LQSGNLIGAW RLRDNTTWSY NSSDRSSGSK 240
20 NKWQHINTWL ERDIIPLRSR LTLGDGYTQG DIFDGINFRG AQLASDDNML PDSQRGFAPV 300
IHGIARSTAQ VTIKQNGYDI YNSTVPPGPF TINDIYAAGN SGDLQVTIKE ADGSTQIFTV 360
PYSSVPLLQR EGHTRYSTA GEYRSGNAQQ EKPRFFQSTL LHGLPAGWTI YGGTQLADRY 420
RAFNFVGIGKN MGALGALSVD MTQANSTLPD DSQHDGQSVR FLYNKSLNES GTNIQLVGYR 480
YSTSGYFNFA DTTYSRMNGY NIETQDGVIO VKPKFTDYNN LAYNKRGLQ LTVTQQLGRS 540
25 STLYLSGSHQ TYWGTSNVDE QFQAGLNTAF EDINWTLNYS LTKNAWQKGR DQMLARNVNI 600
PFSHWLRSDS KSQWRHASAS YSMHDLNLR MTNLAGVYGT LLEDNNLSYS VQTGYAGGGD 660
GNSGSTGYAT LNYRGGYGNA NIGYSHSDDI KQLYYGVSGG VLAHANGVTL GQPLNDTVVL 720
VKAPGAKDAK VENQTGVRTD WRGYAVLPYA TEYRENVAL DTNTLADNVD LDNAVANVVP 780
TRGAIVRAEF KARVGKILM TLTHNNKPLP FGAMVTSESS QSSGIVADNG QVYLSGMPLA 840
30 GKVQVKWGE ENAHCVANYQ LPPESQQQLL TQLSAECR 878
<212> Type : PRT
<211> Length : 878
SequenceName : SEQ ID 23
35 SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
40 <400> PreSequenceString :
MQIIFGEKCV SLLRLFFAAV LMLWCAQTAA YSGQCHTTQG NPYIGVNFGV KTLLEEEENTT 60
GVVVDKIFYQW NESNDYYVSC DCDKDNVRSR RWAFAADSPL VYLDGNWYKI NDYLAQKVL 120
QVKGSSPTAV PFENVGTGAD TRWHICDPGG QRLGGQGASG NSGSFSLKIL QPFVGSVIP 180
PMALARLFEC YNIPAGDSCT TTGTPVLVYY LSGTINSLGS CSVNAGETIE VDLGDVFAAN 240
FRVVGHKPLG ARTAELAIPV RCNTGNAGLV NVNLSLTATT DPSYPQAIKT SRPGVGVVVT 300
45 DSQNNIISPA GGTLPPLSIPD DADSLA 326
<212> Type : PRT
<211> Length : 326
SequenceName : SEQ ID 24
50 SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
55 <400> PreSequenceString :
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RTASLAQDGA TSSAVGFNIQ LNDCTNVAS KAAVAFLGTV IDAGHTNVLA LQSSAAGSAT 120
NVGVQILDRT GAALTLDGAT FSEQTTLNNG TNTIPFQARY YAIQEATPGA ANADATFKVQ 180
YQ 182
<212> Type : PRT
60 <211> Length : 182
SequenceName : SEQ ID 25
SequenceDescription :

Sequence

65 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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 ASAATRTAVE VWTDTTPESN GSTQFHCAQK IPVPVTLPAD TTTQPYDYPL SARMTVAEGR 180
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 5 <212> Type : PRT
 <211> Length : 201
 SequenceName : SEQ ID 26
 SequenceDescription :
 10 Sequence

 <213> OrganismName : Escherichia coli O157:H7
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 NGTAEYSVLN DGYQIVQMGG AANQTTLNNG VLQVYGAAND PTIKGGRLLV EKDGITVLAA 120
 IEKGGLLEVK EGGLAIAVDQ KAGGAIKAST RVMEVFGTNR LGQFEIKNGI ANNMLLENGG 180
 SLRVEENDFA YNTTVDSSGL LEVMDGGTAT GVDKKAGGKL IVSTNALEVS GTNSKGQFSI 240
 KDGVSKNYEL DDGSGLIVME DTQAIDTILD EHATMQSLGK DTGTRVQANA VYDLGRSDQN 300
 GSITYSSKAI SENMVINNGR ANVWAGTMVN VSVRGNDGIL EVMKQPINYA PAMLVGKVVV 360
 20 SEGASLRTHG AVDTSKADVS LENSATWIIA DITTTNQNTN LNLANLAMSG ANVIMMDES 420
 TRSSVTASAE NFTTLTNTNL SGNGNFYMRD DMANHQSDDL NVTGQATGDF KIFVTDGAS 480
 PAAGDSLTLV TTGGGDAFT LGNAGGVVDI GTYEYTLNLD GNHSWSLAEN RAQITPSTD 540
 VLNMAAAQPL VFDAELDTVR ERLGSVKGVV YDTAMWSSAI NTRNNVTDA GAGFEQTLTG 600
 LTLGIDSRFS REESSTIRGL FFGYSHSDIG FDRGGKGNVD SYTLGAYAGW EHONGAYVDG 660
 25 VVKVDRFANT IHGKMSNGAT AFGDYNNGA GAHVESGFRW VDGLWSVRPY LAFTGFTTDG 720
 QDYTLNGMR ADVGNTRLR AEAGTAVSYH MDLQNGTTLE PWLKAAVRQE YADSNQVKVN 780
 DDGKFNNDDA GTRGVYQAGI RSSFTPTLSG HLSVSYNGA GVESPWNTQA GVVWTF 836
 <212> Type : PRT
 30 <211> Length : 836
 SequenceName : SEQ ID 27
 SequenceDescription :
 Sequence
 35 -----
 <213> OrganismName : Escherichia coli O157:H7
 <400> PreSequenceString :
 MQRKGNKLLI QLCSVILLFF TTSWYALANE CYIERNAEGD YHMKISSTQL SLASQMVEVP 60
 TEIAEATWDV NIQLRGDAIG CKSLGDSKAV HFLNTADPSL ISTYTTTNGA ALLKTTVPPI 120
 40 VYSVELLCLS CGAADELDLW LPAQSGADNF IPSTQTKWAY EYSDQSWYLR FRLFITPEFK 180
 PKNGVSSGTT IAGKIASWYI GTNDQPWINF YIDNDSLKFF VDEPTCATVA LAQDQGNVSG 240
 NQVTLGNSYV SEVKNGLTRE IPFSIRAAYC YASKITVKLK AANKPSDATL VGKTTGSASG 300
 VAVKVNSTYD NSKVLLKADG SNTVDYNFAA WSNLLFLPF TAQLVPDGSQ NAVGVGTFSG 360
 NATFSFTYE 369
 45 <212> Type : PRT
 <211> Length : 369
 SequenceName : SEQ ID 28
 SequenceDescription :
 Sequence
 50 -----
 <213> OrganismName : Escherichia coli O157:H7
 <400> PreSequenceString :
 MYQFTHQKSR IPKKTLLAAC CALFYSSNGA AADTVEYDSS FLMGTGASTI DVKRYAQGNP 60
 55 TPPGLYNVRV FVNGQATSSL EIPFVDIGEN SAAACLTHKN LAQLHIKQPE QPVTLLAREG 120
 EEEDCLDLAK SYEKADVCFD GSDQFLDLTI PQAYVLKSYG GYVDPSSLWES GINAATLAYT 180
 LNAYHTSSDN DNSDSVYGAF NSGINLGAWH FRARGYNWT TDNGSDFDFQ DRYLQRDIPA 240
 IRSQIIMGDA YTTGETFDSV NVRGVRLYSD SRMLPSALAS YAPTIRGVAN SNAKVTVTQS 300
 GYKIYETTVP PGEFVIDDIS PSGFGSELVV TIEADGSKR TFTQPFSSVV QMQRPGVGRW 360
 60 DFSAGKVIDD SLRSEPMMGQ ASYYYGLNNL FTGYTGIIQT DNNYLALGLL VGINTSIGAF 420
 AVDVTHSRAE IPDDKTYQGQ SYRVTWKLF QDTGTSFNLA AYRYSTQDYL GLHDALVLID 480
 DAKHLSADED KNTMQTYSRM KNQFTVSINQ PLNIAYEDYG SLFISGSWTY YWAANNRTE 540
 YNVGYSKSVS WGSFVSNLQR SWNEDGEKDD AMYVSVSVPI ENILGKGRKS SGFRNLNTQL 600
 NTDFDGSQHL NVNSSGNTEN NLVNVSVNAG YSLDKNAGDL ASVGGYLYE SGLGGISASA 660
 65 SATSDNSQQY SISTDGGFVL HSGGLTFTNN SFSSNDTLVL INALGAKGAR INNSNNEIDR 720
 WGYAVTSSVS PYRENRVGLN IETLENDVEL KSTSATTVPR SGSVVLTRFE TDEGRSAVLN 780
 ITAANGKSIP FAAEVYQGEV MIGSMGQGGQ AFVRGINDSG ELIVRWYENN QTIDCKLHYQ 840

FPAQPQTQGS TNTLLLNLT CQVANH 866
<212> Type : PRT
<211> Length : 866
SequenceName : SEQ ID 29
SequenceDescription :

5 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
10 MKFKRLLHSG IASLSLVACG VNAATDLGPA GDIHFSITIT TKACEMEKSD LEVDMGMTML 60
QKPAAVGTVL SKKDFTIELK ECDGISKATV EMDSQSDSDD DSMFALEAGG ATGVALKIED 120
DKGTQQVPKG SSGTPIEWAI DGETTSLHYQ ASYVVVNTQA TGGTANALVN FSITYE 176

15 <212> Type : PRT
<211> Length : 176
SequenceName : SEQ ID 30
SequenceDescription :

20 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
25 MKYNNIIFLG LCLGLTTYSA LSADSVIKIS GRVLDYGCTV SSDSLNFTVD LQKNSARQFP 60
TTGSTSPAVP FQITLSECSK GTTGVRVAFN GIEDAENNTL LKLDEGSNTA SGLGIEILDG 120
NMRPVKLNDL HAGMQWIPLV PEQNNILPYS ARLKSTQKSV NPGLVRASAT FTLEFQ 176

30 <212> Type : PRT
<211> Length : 176
SequenceName : SEQ ID 31
SequenceDescription :

Sequence

35 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKWRKRGYLL AAILALASAT IQAADVTITV NGKVVAKPCT VSTTNATVDL GDLYSFSLMS 60
AGAASAWHDV ALELTNCPVG TSRVTASFSG AADSTGYKN QGTAQNIQLE LQDDSGNTLN 120
TGATKTVQVD DSSQSAHFPL QVRALTVNGG ATQGTIQAVI SITYTYS 167

40 <212> Type : PRT
<211> Length : 167
SequenceName : SEQ ID 32
SequenceDescription :

45 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
50 MKRAPLITGL LLISTSCAYA SSEGCCADST SGATNYSSVV DDVTVNQTDN VTGREFTSAT 60
LSSTNQYAC SCSAGKAVKL VYMVSPVLTT TGHQTGYKYL NDSLDIKTMN RPNPND 117

<212> Type : PRT
<211> Length : 117
SequenceName : SEQ ID 33
SequenceDescription :

55 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
60 MKKALLAAL VMASGSALAV DGGHIDFNGM VQSGTCKVGV VDTGMHSTTT DGVVTLDTAN 60
VTDTFAEVSA TAVGLLPKEF MISVECDPGA PKNAELTMGS ASYANTSGTL NNNMNITVNG 120
IAPQNVNIA VHNMKNKAGA ABEIKQVHMNN SSEVQELTLD AEGKGQYVFN ASYVKAPNSP 180
AVTAGHVTN ALYTVAYK 198

65 <212> Type : PRT
<211> Length : 198
SequenceName : SEQ ID 34

SequenceDescription :

Sequence

5 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKPNMIVGAL ALTSVFMAGH LQAADGTVHF RGEIIDSTCE VTPETKDQVV DLGKVNRTAF 60
SGVDDVAAPT AFSIDLTQCP ETFKSAAIRF DGNEDAHGNG NLAIGTPLDN SNDAAAGISP 120
SDNSGDYTGGA GAVSAAKGVA IRLYNRADNT QVKLYENSAS TPISNGNASM KFMARYIATE 180
10 TTIDPGTANA DSQFTVEYIK 200
<212> Type : PRT
<211> Length : 200
SequenceName : SEQ ID 35
SequenceDescription :

Sequence

20 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MPIFQREGHL KYSFAAGEYQ AGNYDSASPR FGQLDLIYGL PWGMTAYGGV LISNNYNAFT 60
LGIGKNFGYI GAISIDVTQA KSELNNDRDS QGQSYRFLYS KSFESGTDPR LAGYRYSTSG 120
FYTFQBATDV RSDADSDYNR YHKRSEIQGN LTQQLGAYGS VYLNLTQQDY WNDAGKQNTV 180
SAGYNGRIGK VSYSAISWN KSPWDESDR LWSFNISVPL GRAWSNYRVT TDQDGRTNQQ 240
VGVSGTLLED RNLSYSVQEG YASNGVGNNG NANVGQGGG GNVNVGYSYG KDYRQLNYSV 300
25 RGGVIVHSEG VTLSQLGET MTLISVPCAR NARVVNNGGV QVDWMGNAIV PYAMPYRENE 360
ISLRSDSLGD DVDVENAFQK VVPTRGAIVR ARFDTRVGYR VLMTLLRSAG SPVPPGATAT 420
LITDKQNEVS SIVGEEGQLY ISGMPEEGRV LIKWGNDASQ QCVAPYKLSL ELKQGGIIPV 480
SANCQ 485
<212> Type : PRT
30 <211> Length : 485
SequenceName : SEQ ID 36
SequenceDescription :

Sequence

35 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSGYTVKPPT GDSNEQTQFI DYFNLFYSKR DQEQISISQQ LGNYGATFFS ASRQSYWNTS 60
RSDQQISFGL NVPFGDITTS LNYSYSNNIW QNDRDHLLAF TLNVPPFSHW RTDSQSAFRN 120
40 SNASYMSND LKGGMTNLSG VYGTLLPDNN LNYSVQVGN HGGNTSSGTS GYSTLNRYGA 180
YGNTNVGYSR SGDSSQIYYG MSGGIIAHAD GITFGQPLGD TMVLVKAPGA DNVKIENQIG 240
IHTDWRGYAI LPFATEYREN RVALNANSLA DNVELDETVV TVIPTHGAIA RATFNAQIGG 300
KVLMTLKYGN KSVPPGAIVT HGENKNGSIV AENGQVYLTG LPQSGKLQVS WGNDRKNSNCI 360
VDYKLPEVSP GTLLNQQTAI CR 382
45 <212> Type : PRT
<211> Length : 382
SequenceName : SEQ ID 37
SequenceDescription :

Sequence

50 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSALYERSQL TQVMISSAPA TAETMEKAIEY LRLDCTIKEV QFTAGQKQDI DVTTLCSSTEQ 60
55 ENINGLGASS EISMSGNFYL NQAQNALRDA YDNDTVYAFK VQFPGSGKGFK FLAEVRQHTW 120
SSGTNGVVAA TFSRLKGGK VSYVPLAFV KNLDKTLTVN TGALLTMSVS VNGGTPPYKH 180
AWKKDGPVE GQTTDTFSKP GAQSGDKGAY TCEVTDSAEQ PQSITSDACT VTVNGAGG 238
<212> Type : PRT
60 <211> Length : 238
SequenceName : SEQ ID 38
SequenceDescription :

Sequence

65 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

MRNKPFFYLLC AFLWLAVSHA LAADSTITIR GYVRDNGCSV AAESTNFTVD LMENAAKQFN 60
NIGATTPVVP FRILLSPCGN AVSAVKVGFT GVADSHNANL LALENTVSAA SGLGIQLLNE 120
QQNQIPLNAP SSAISWTTLT PGKPNTLNFY ARLMATQVPV TAGHINATAT FTLEYQ 176

5 <212> Type : PRT
<211> Length : 176
SequenceName : SEQ ID 39
SequenceDescription :

10 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
15 MNKSVVSISA AMLVLLCQPV MGSEISPATP .SDEDNYTTFDP QLFGRGSRFSQ SSLAKLITRE 60
SVAPGNKYMD IYTNNKLSGS WNVTFKEAAD GRVLPCLTPE VADAIGLKTG EDKGEKDPVC 120
TFAKELAPGI TSQTQLSQLR LDLSVPQSQL ISRPRGYVPP SELDTGASLA FMNYIANYYN 180
VAYSGQNAHS QRSIWASFNG GINLGAWQYR QLSNMTWDND KGNQWNNIRS YLQRPLPAIN 240
SQLMMGLLIT SGRFFSGLSY HGVSLATDER MLPDSMRGYA PTIRGVAATN ARVSVMQNGH 300
ETIYQTTVAPG PFEINDLYPT SYSGDLDTVT TEANGAVSRF SVPFSAVPES MRPGTSRYNV 360
20 EVGKTQDSGD DSMFGDLTWQ HGMTNTLTFTN SGSRIADGYQ ALMLGGVYGS SLGAFGANLT 420
WSHARVPES AQSGWMSQLT WSKTFQPTST TVSLAGYRYS TSGYRDLADV LGERHAASNK 480
QSWDSSQWRQ QSRFDLTLSQ SLANYGNLFV SGSTQNYRGG KSRDTQLQLG YSNSFSHGSI 540
MNLVSGRQRM GGYKDNSDDM QTVTSLSFSF PLGGNGPRVP SLSNSWTHST DGSSQLQSSL 600
TGMLDEAQT NYSLNVMRDQ QYKQTTLSGN MQKRFSQTTV GLNASKGQDY WQASGNVQGA 660
25 MAVHGGGITF GPYLGETFAL VEAKGAEGAK VYNSSQLEIN DSGYALVPAV TPYRYNRISL 720
DPQGMDSGAE LVDSEKQVAP VAGAAVKVIF RTRPGKALLI KSRMADGSEL PMGADVLDEN 780
NTVVGIAQGQ GQIYLRTETQ KGHLSVRWGE GANDSCQLPF DISGKDSNSP IIRLNETCQS 840

<212> Type : PRT
30 <211> Length : 840
SequenceName : SEQ ID 40
SequenceDescription :

Sequence

35 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MCLAACFLTL LPGAFAVAASW TSPGFPAFSE QGTGTFVSHA QLPKGTRPLT LNFDQQCWQP 60
ADAIKLNQML SLQPCSNTPP QWRLFRDGKY TLQIDTRSGT PTLMISIQNA AEPVANLVRE 120
40 CPKWDGLPLT LDVSATFPEG AAVRDYYSQQ IAIKNGQIT LQPAATSNGL LLLERAETDA 180
SAPFDWNNAT VYFVLTRDFE NGDPSNDQSY GRHKDGMAEI GTFHGGDLRG LTNKLDYLQQ 240
LGVNALWISA PFEQIHGWVG GGTKGDFPHY AYHGYTQDW TNLDANMGNE ADLRTLVD SA 300
HQRGIRILFD VVMNHTGYAT LADMQEYQFG ALYLSGDEVK KTLGERWSDW KPAAGQWHS 360
FNDYINFSDK TGWDKWWGKN WIRTDIGDYD NPGFDDLTMS LAFLPDIKTE STTASGLPVF 420
45 YKNKTDTHAK AIDGFTPRDY LTHWLSQWVR DYGIDGFRVD TAKHVELPAW QQLKTEASAA 480
LREWKANPD KALDDKPFWM TGEAWGHGVM QSDYYRHGFD AMINFQYQEQ AAKAVDCIAQ 540
MDTTWQMAE KLQGFNVLSY LSSHDTLRLFR EGGDKAAELL LLAPGAVQIF YGDESSRPFG 600
PTGSDPLQGT RSPMNWQDVS GKSAANVAHW QKISQFRARH PAIGAGKQTT LSLKQGYGFV 660
REHGDDKVLV IWAGQQ 676

50 <212> Type : PRT
<211> Length : 676
SequenceName : SEQ ID 41
SequenceDescription :

55 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
60 MPQRHHQGHK RTPKQLALII KRCLPMVLTG SGMLCTTANA EBYFDPIML ETTKSGMQTT 60
DLSRFSKYA QLPGTYQVDI WLNKKKVSQK KITFTANAEQ LLQPQFTVEQ LRELGIKVDE 120
IPALAEKDD SVINSLEQII PGTAAEFDNF HQRNLNLSIP IALYRDARGY VSPSRWDDGI 180
PTLFTNYSFT GSDNRYRQGN RSQRQYLNMQ NGANFGPWRL RNYSTWTRND QASSWNTISS 240
YLQRDIKALK SQQLLGESAT SGSIFSSYNF TGVLASDDN MLPNSQRGFA PTVRGIANSS 300
AIVTIRNGY VIYQSNVPAG AFEINDLYPS SNSGDLEVTI EESDGTQRRF IQPYSSLPM 360
65 QRPGLHKYSA TAGRYRADAN SDSKEPEFAE ATAIYGLNNT FTLYGGLLGS EDYYALGIGI 420
GGTLGALGAL SMIRNADTQ FDNQHSFHY PETNTNIAVS YYRYTNDGYF 480
SFDEANTRNW DYNRQKSEI QFNISQTIFD GVSLYASGSQ QDYWGNNEKN RNISVGVSQ 540

QWIGIGYSLNY QYSRYTDQNN DRALSLNLISI PLERWLPRSR VSYQMTSQKD RPTQHEMRID 600
GSLDDGRLS YSLEQSLDDD NNHNSSVNAS YRSPYGTFS A GYSYGNDSQ YNYGV TGGVV 660
IHPHGVTL SQ YLGNALID ANGASGVRIQ NYPGIATDPF GYAVVPYLT YQENRLSVDT 720
TQLPDNDLE QTTQFVVPNR GAMVAARFNA NIGYRVLVTV SDRNGKPLPF GALASNDDTG 780
5 QQSIVDEGGI LYLSGISSKS QSWTVRWGNQ ADQQCQFAFS TPDSEPTTSV LQGT AQCH 838

<212> Type : PRT
<211> Length : 838
SequenceName : SEQ ID 42
10 SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
15 <400> PreSequenceString :
MMFRNRILLI FILWANFTWA GCRTTASLNI TDGINVGEIL ANETSFSKSV VFTGISCDTS 60
TDKIVYKNIQ SDWVEVGPFG NGEKLVKIE SLGKTS DTIG KSSNAQAVLP YVVKIARGTP 120
DFTGERKSTW FISTVIANI GGESSSIDF WLGICKALKF NWCVN YLTSK LAGDTFTLGL 180
NISYYPKNTT CKPENTVIKV DDIALFQLRN QGKIAANSKE GTITLKCDNL FGDKKQASRN 240
20 MVVYLSSSDL VKGSNTILRG KTDNGVGFVL DLTEPPKGTE AAIKISANGD QGAATSLWKT 300
DKPGVSLNSN IINIPVMASY VYDEKKVKS GALEATALIN VKYD 344

<212> Type : PRT
<211> Length : 344
SequenceName : SEQ ID 43
25 SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
30 <400> PreSequenceString :
MIKKASLLTA CSVTAFAWA QDTSPDTLVV TANRFEQPRS TVLAPTTVVT RQDIDRWQST 60
SVNDVLRRLP GVDITQNGGS QQLSSIFIRG TNASHVLVLI DGVRNLNLAGG SGSADLSQFP 120
IALVQRVEYI RGRPSAVYGS DAIGGVNII TTRDEPGTEI SAGWGSNSYQ NYDVSTQQQL 180
GDKTRVTLLG DYATHGYDV VAYGNTGTQA QPDNDGFLSK TLYGALEHNF TDAWSGFVRG 240
35 YGYDNRTNYD AYYSPGSPLV DTRKLYSQSW DAGLRYNGEL IKSQLITSYS HSKDYNYPH 300
YGRYDSSATL DEMKQYTVQW ANNIIIGHGN VGAGVDWQKQ STAPGTAYVK DGYDQRNTGI 360
YLTGLQQVGD FTFEGAARSD DNSQFGRHGT WQTSAGWEFI EGYRFIASYG TSYKAPNLGQ 420
LYGFYGNPNL DPEKSKQWEG AFEGLTAGVN WRISGYRNDV SDLIDYDDHT LKYYN EGKAR 480
IKGVEATANF DTGPLTHTVS YDYVDARNAI TDTPLLRRAK QQVKYQLDWQ LYDFDWGIT Y 540
40 QYLGTRYDKD YSSYPYQTVK MGGVSLWDLA VAYPVTSHLT VRGKIANLFD KDYETVYGYQ 600
TAGREYTL SG SYTF 614

<212> Type : PRT
<211> Length : 614
SequenceName : SEQ ID 44
45 SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
50 <400> PreSequenceString :
MKNKLLFMML TILGAPGIAA AAGYDLANSE YNFAVNELSK SSFNQAAIIG QAGTNNSAQL 60
RQGGSKLLAV VAQEGSSNRA KIDQTGDYNL AYIDQAGSAN DASISQ GAY NTAMIIQKGS 120
GNKANITQYG TQKTAIVVQR QSQMAIRVTQ R 151

<212> Type : PRT
55 <211> Length : 151
SequenceName : SEQ ID 45
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
60 <400> PreSequenceString :
MNIFAYLLVL VFSMSMSSA FASVMTGTR IIFPGDAKEK TIQLRNTSDQ PYIINI HVED 60
ERGS DKNVFP MPTPTFRME AAAGQALRL L YTGNL PQDR ES VFWFSFSQ LPYLNKNDKS 120
65 QNQLILALTN RVKIFYRPSS IVGKSSDAPK NLTYQVKQNR IEVTNPTGYY VTIRAAELLN 180
NGKKVPLANS VMIAPQSTTE WTLPSGISVA PGAQIHLTV NDYGVNVTSE HAL 233

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<212> Type : PRT
<211> Length : 233
      SequenceName : SEQ ID 46
      SequenceDescription :
5
Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
10 MKRLHKRFLI ATFCALLTAT LQAADVITIV NGRVVAKPCT IQTKEANVNI GDLYTRNLQQ      60
   PGSASGWHNI TSLTDCPAE TSAVTAIVTG STDNTGYYKN EGTAENIQIE LRDDQDATLK      120
   NGDSKTVIVD EITRNAQFPL KARAITVNGN ASQGTIEALI NVIYTWQ      167
<212> Type : PRT
<211> Length : 167
15      SequenceName : SEQ ID 47
      SequenceDescription :

Sequence
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20 <213> OrganismName : Escherichia coli O157:H7
   <400> PreSequenceString :
   MRAKLLGIVL TTPAIASSFA STETLSFTPD NINADISLGT LSGKTKERVY LAEEGGRKVS      60
   QLDWKFNNAI IIKGAINWDL MPQISIGAAG WTTLGSRRGN MVDQDWMDS NPGTWIDESR      120
   HPDTQLNYAN EFDLNIKGWL LNEPNYRLGL MAGYQESRYS FTARGGSYIY SSEEGRDDI      180
25   GSFPNGERAI GYKQRFKMPY IGLTGSYRYE DFELGGTFKY SGWVEASDND EHYDPGKRIT      240
   YRSKVVDQNY YSVSVNAGYY VTPNAKVYVE GTWNRVTNKK GNTSLYDHND NTSDYSKNGA      300
   GIENYNFITT AGLKYTF      317
<212> Type : PRT
<211> Length : 317
30      SequenceName : SEQ ID 48
      SequenceDescription :

Sequence
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35 <213> OrganismName : Escherichia coli O157:H7
   <400> PreSequenceString :
   MFFKRGKILS AGRLNKKSILG IVMLLSVGLL LAGCSGSKSS DTGTYSGSVY TVKRGDTLYR      60
   ISRTTGTSVK ELARLNGISP PYTIEVGQKL KLGGAKESSS TRKSTAKSTT KTASVTPSSA      120
   VPKSSWPPVG QRCNLWPTTG KVIMPYSTAD GGNKGIDISA PRGTPPIYAG AGKVYVVGNO      180
40   LRGYGNLIMI KHSEDIYITAY AHNDTMLVNN GQSVKAGQKI ATMGSTDAAS VRLHFQIRYR      240
   ATAIDPLRYL PPQGSKPKC      259
<212> Type : PRT
<211> Length : 259
45      SequenceName : SEQ ID 49
      SequenceDescription :

Sequence
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50 <213> OrganismName : Escherichia coli O157:H7
   <400> PreSequenceString :
   MPTPNPLAPV KGAGTTLWVY NGNGDPYANP LSDNDWSRLA KVKDLTPGEL TAESYDDSYL      60
   DDEDADWAAT GQGQKSAGDT SFTLAWMPGE QGQALLAWF NEGDTRAYKI RFPNGTVDVF      120
   RGWVSSIGKA VTAKEVITRT VKVTNVGRPS MAEDRSTVTA ATGMTVTPAS TSVVKGQSTT      180
   LTVAFAQPEGA TDKSFRAVSA DTKKATVSVS GMTITVKGVA AGKVNIPVVS GNGEFAAVAE      240
55   INVTAS      246
<212> Type : PRT
<211> Length : 246
      SequenceName : SEQ ID 50
      SequenceDescription :

60 Sequence
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   <213> OrganismName : Escherichia coli O157:H7
   <400> PreSequenceString :
65   MSALYERSQL TQVMISSAPA TAETMDKAEY LRLDCTIKEV QFTAGQKQDI DVTTLCSREQ      60
   ENINGLGASS EISMSGNFYL NQAQNALRDA YDNDALYAFK VLFPSGKGFK FLAEVRQHTW      120
   SSGTNGVVAA TFSRLKKGKP VSFVVPLAFV KNLDKTLTVN TGALLTMSVS ANGGTPPYKY      180
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AWKKDGPVD GQTTDTFSKP GAQSADAGKY TCVVTDSAEK AQSPTSVECT VIVSAAAG 238

<212> Type : PRT
<211> Length : 238
5 SequenceName : SEQ ID 51
SequenceDescription :

Sequence

10 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKSTLALVV MGIVASASVQ AAEIYNKDGN KLDVYGKVK MHYMSDND SK DGDQSYIRFG 60
FKGETQINDQ LTGYGRWEAE FAGNKAESDT AQQKTRLAFA GLKYKDLGSF DYGRNLGALY 120
DVEAWTDMFP EFGGDSSAQT DNFMTKRASG LATYRNTDFF GVIDCLNLTL QYQGYNENRD 180
15 VKKQNGDGFG TSLTYDFGGS DFAISGAYTN SDRTNEQNLO SRGTGKRAEA WATGLKYDAN 240
NIYLATFYSE TRKMTPTGG FANKTQNF EA VAQYQDFDGL RPSLGYVLSK GKDIEGIGDE 300
DLVNYIDVGA TYYFNKNMSA FVDYKINQLD SDNKLININD DIVAVGMTYQ F 351

<212> Type : PRT
20 <211> Length : 351
SequenceName : SEQ ID 52
SequenceDescription :

Sequence

25 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRVKHAVVLL MLISPLSWAG TMTFQFRNPN FCGPNPNNAGF LLNSAQANNS YKDPSYNDDF 60
GIETPSALDN FTQAIQSQIL GGLLSNINTG KPGRMVTNDY IVDIANRDGQ LQLNVTDRKT 120
30 GQTSTIQVSG LQNNSTDF 138

<212> Type : PRT
<211> Length : 138
SequenceName : SEQ ID 53
SequenceDescription :

35 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
40 MKRKVLAMLV PALLVAGAAAN AAEIYNKDGN KLDLYGKVVAG LHYFSDDASS DGDMSYARIG 60
FKGETQIADQ FTGYGQWEFN IGANGPESDK GNTATRLAFA GFGFGQNGTF DYGRNYGVVY 120
DVEAWTDMFP EFGGDTYAGA DNFMNNGRANS VATYRNNNGFF GQVDGLNFAL QYQGNNEKSG 180
LFDQEGSGNG NGRKLAKENG DGSVCPLPMT LTLV 214

<212> Type : PRT
45 <211> Length : 214
SequenceName : SEQ ID 54
SequenceDescription :

Sequence

50 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNTVTLEGGT FNNNGTLNDV VKIEKNSNAV INNTGSLSTL QLHDGTVNNS GIASARVNAQ 60
GDAVFNNLAG GEARKGAILY NSAVVNNAGT WKMGYQDENN NAGTLDIDDK STFNNSGKLI 120
55 LDNSKNAIRF QGSNANATLY NTGEMTLDAAL LGAGAILYDD GASEFINKGV VDAKVTVAVS 180
TAGATESDAF LWNQDGGVIN FDKDNASAVK FTHNNYVALN DGVMNISGNN AVAMEGDKNA 240
QLVNNGVINL GTEGTTDTGL TGMQLDANAT ADAVIENNGT INIFANDSFA FSVLGTGEGHI 300
VNNGTIVVIAD GVTGSGLIKQ GDSVNVEGVN GNSGNNTVEVH YTDYTLDPMP NTYTTSPFSE 360
TTDSGSSDGS SNNLNGYIVG TNVDGSAGKL KVNNASMNGV GINTGFAAGT ADTTSVFDNV 420
60 VEGINLTAD AITSTSVVWT AKGSTDASGN VDVIMSKNAY TDVATDASVN DVAKALDAGY 480
TNNELYTSLN VGTAEELNSA LKQVSGSQAT TVFREARVLS NRFSMLADAA PKVGNGLAFN 540
VVAKGDPRAE LGNNTEYDML ALRKTVDLSE SQSMSLEYGI ARLDGDGAQK AGDNGVTGGY 600
SQFFGLKHQM SFDNGMRWNN ALRYDVHNL DSSRSVAYGDV SKTADTDVKQ QYLELRSEGA 660
KTFEPREGLK ITPYAGVKLR HSLEGGYQER NAGDFNLMSN SGSETAVDSI VGLKLDYAGK 720
65 GGSANATLE GGPNLSSYSKS QRTASLAGAG SQHFNVDGQ KGGGINSLAS VGVKYSKES 780
SLNLDAYHWK EDGISDKGVM LNFKKTF 807

<212> Type : PRT

<211> Length : 807
SequenceName : SEQ ID 55
SequenceDescription :

5 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MLNGISNAAS TLGRQLVGIA SRVSSAGGTG FSVAPQAVRL TPVKVHSPFS PGSSNVNART 60
10 IFNVSSQVTS FTPSRPAPPP PTSGQASGAS RPLPPPIAAL KEHLAAYEKS KGPEALGFKP 120
ARQAPPPPTS GQASGASRPL PPIAQALKEH LAAYEKS KGP EALGFKPARQ APPPPTSGQA 180
SGASRPLPPI AQALKEHLAA YEKS KGP EALGFKPARQ APPPPTSGQA 240
AYEQSKKG 248
<212> Type : PRT
15 <211> Length : 248
SequenceName : SEQ ID 56
SequenceDescription :

Sequence

20 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNKKIHSLAL LVNLGIYGVA QAQEPDTPV SHDDTIVVTA AEQNLQAPGV STITADEIRK 60
NPVARDVSEI IRTMPGVNLT GNSTSGQRGN NRQIDIRGMG PENTLILIDG KPVSSRNSVR 120
25 QGWRGERDTR GDTSWVPPEM IERIEVLRGP AAARYGNAA GGVVNIITKK GSGEWHGSWD 180
AYFNAPEHKE EGATKRTNFS LTGPLGDEFS FRLYGNL DKT QADAWDINQG HQSARAGTYA 240
TTLPAGREGV INK DINGVVR WDFAPLQSL E LEAGYSRQGN LYAGDTQNTN SDAYTRSKYG 300
DETNRLYRQN YSLTWNGGWD NGVTTSNWVQ YEHTRSRIP ELAGGTEGK FNEKATQDFV 360
DNDLDDVMLH SEVNLPIDFL VNQTLTLGTE WNQQRMKDLS SNTQALTGTN TGG AIDGVSA 420
30 TDRSPYSKAE IFSLFAENNM ELTDSTIVTP GLRFDHHSIV GNNWSPALNI SQGLGDDFTL 480
KMGIARAYKA PSLYQTNPNY ILYSKGQGCY ASAGGCYLQG NDDLKAETSI NKEIGLEFKR 540
DGWLAGITWF RNDYRNKIEA GYVAVGQNAV GTDLYQWDNV PKAVVEGLEG SLNVPVSETV 600
MWTNNITYML KSENKTTGDR LSIIPEYTLN STL SWQARED LSMQTTFTWY GKQ QPKKYN Y 660
KGQPAVG PET KEISPYSIVG LSATWDVTKN VSLTGGVDNL FDKRLWRAGN AQT TGDLAGA 720
35 NYIAGAGAYT YNEPGRTWYM SVNTHF 746
<212> Type : PRT
<211> Length : 746
SequenceName : SEQ ID 57
SequenceDescription :

40 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
45 MGRFSLRYK KLSYRFVFLT LAGCSSVGNO SLKNETQESV KTKIVKGKTT KQDVLASFGE 60
PDSRSLIDGE EQW SYTYMNS QSKATSFIPV VGLLAGGADS QTKSLTVSFK GEKVSTYIFN 120
AGTSNVKTGI F 131
<212> Type : PRT
<211> Length : 131
50 SequenceName : SEQ ID 58
SequenceDescription :

Sequence

55 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKIACLSAL AAVLAFTAGT SVAATSTVTG GYAQSDAQGO MNKMGGFNLK YRYEEDNSPL 60
GVIGSFTYTE KSRTASSGDY NKNQYYGITA GPAYRINDWA SIYGVGVGY GKFTTEYPT 120
YKHTSDYGF SYGAGLQFNP MENVALDFS Y EQSRIRSV DV GTWIAGVGYR F 171
60
<212> Type : PRT
<211> Length : 171
SequenceName : SEQ ID 59
SequenceDescription :

65 Sequence

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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
5 MKSIATLVVC AISGIACVNL SAHAAEGEHT ISLGIAHFQF PGLKDFVKDA TAHNRETFSH 60
  FVNRNYFSSL GEYTDGRVSG YEGKDKNPQG INIRYRYEIT DDFGVITSFT WTRSLTNSQT 120
  FIDVQSADHT RRIKNPAASA RTDIRANYWS LLAGPSWRVN QYMSLYAMAG MGVAKVSADL 180
  KIKDNINSSG GFSESNSTKK TSLAWAAGAQ FNLNESVTL D VAYEGSGSGD WRTSGVTAGI 240
  GLKF 244
<212> Type : PRT
<211> Length : 244
10 SequenceName : SEQ ID 60
  SequenceDescription :

Sequence
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15 <213> OrganismName : Escherichia coli O157:H7
  <400> PreSequenceString :
  MRKLYAAILS AAICLTVSGA PAWASEQQAT LSAGYLHVST NAPGSDNLNG INVKYRYEFT 60
  DTLGLVTSFS YAGDRNRQIT RYSDTRWHED SVNRNRWFSVM AGPSVRVNEW FSAYAMAGVA 120
  YSRVSTFSGD YLRVTDNKGK THDVLTSDD GRHSNTSLAW GAGVQFNPTE SVAIDIAIEG 180
  SSGSDWRTDG FIVGVGYKF 199
  <212> Type : PRT
  <211> Length : 199
    SequenceName : SEQ ID 61
    SequenceDescription :

25 Sequence
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  <213> OrganismName : Escherichia coli O157:H7
  <400> PreSequenceString :
  30 MRKLYAAILS AAICLAVSGA PAWASEQQAT LSAGYLHART SAPGSDNLNG INVKYRYEFT 60
    DTLGLVTSFS YAGDKNRQLT RYSDTRWHED SVNRNRWFSVM AGPSVRVNEW FSAYAMAGVA 120
    YSRVSTFSGD YLRVTDNKGK THDVLTSDD GRHSNTSLAW GAGVQFNPTE SVAIDIAIEG 180
    SSGSDWRTDG FIVGVGYKF 199
    <212> Type : PRT
  35 <211> Length : 199
    SequenceName : SEQ ID 62
    SequenceDescription :

Sequence
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40 <213> OrganismName : Escherichia coli O157:H7
  <400> PreSequenceString :
  MRKLYAAILS AAICLAVSGA PAWASEQQAT LSAGYLHART SAPGSDNLNG INVKYRYEFT 60
  DTLGLVTSFS YAGDKNRQLT RYSDTRWHED SVNRNRWFSVM AGPSVRVNEW FSAYAMAGVA 120
  45 YSRVSTFSGD YLRVTDNKGK THDVLTSDD GRHSNTSLAW GAGVQFNPTE SVAIDIAIEG 180
    SSGSDWRTDG FIVGVGYKF 199
    <212> Type : PRT
  <211> Length : 199
    SequenceName : SEQ ID 63
  50 SequenceDescription :

Sequence
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  <213> OrganismName : Escherichia coli O157:H7
  <400> PreSequenceString :
  55 MRKLYAAILS AAICLAVSGA PAWASEQQAT LSAGYLHART SAPGSDNLNG INVKYRYEFT 60
    DTLGLVTSFS YAGDKNRQLT RYSDTRWHED SVNRNRWFSVM AGPSVRVNEW FSAYAMAGVA 120
    YSRVSTFSGD YLRVTDNKGK THDVLTSDD GRHSNTSLAW GAGVQFNPTE SVAIDIAIEG 180
    SSGSDWRTDG FIVGVGYKF 199
  60 <212> Type : PRT
  <211> Length : 199
    SequenceName : SEQ ID 64
    SequenceDescription :

65 Sequence
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  <213> OrganismName : Escherichia coli O157:H7
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<400> PreSequenceString :
MVMSQKTLFT KSALAVAVAI ISTQAWSAGF QLNEFSSSSGL GRAYSSEGAI ADDAGNVSRN 60
PALITMFDPR TFSAGAVYID PDVNISGTSP SGRSLKADNI APTAWVPNMH FVAPINDQFG 120
WGASITSNYG LATEFNDTYA GGSVGGTTDL ETMNLNLSGA YRLNNAWSFG LGFNAVYARA 180
5 KIERFAGDLG QLVAGQIMQS PAGKTPQGQA LAATANGIDS NTKIAHLNGN QWGFQWNAGI 240
LYELDKNNRY ALTYSSEVKI DFKGNYSSDL NRVFNNGYGLP IPTATGGATQ SGYLTINLPE 300
MWEVSGYNRV DPQWAIHYSL AYTSWSQFQQ LKATSTSGDT LFQKHEGFKD AYRIALGTTY 360
YYDDNWTFRF GIAFDDSPVP AQNRSISIPD QDRFWLSAGT TYAFNKDASV DVGVSVMHGO 420
SVKINEGPYQ FESEKAWLF GTNFNAYF 448

10 <212> Type : PRT
<211> Length : 448
SequenceName : SEQ ID 65
SequenceDescription :

15 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MAFSQAVSGL NAAATNLVDI GNNIANSATY GFKSGTASFA DMFAGSKVGL GVKVAGITQD 60
20 FTDGTTTNTG RGLDVAISQN GFFRLVDSNG SVFYSRNGQF KLDENRNLVN MQGLQLTGYP 120
ATGTPPTIQQ GANPTNISIP NTLMAAKTTT TASMQINLNS SDPLPSVNAF DASNADSYNK 180
KGSYTVFDSQ GNAHDMSVYF VKTGDNNWQV YTDSSDPTG TAEPAMKLVF NANGVLTSNP 240
TENITTGAIN GAEPATFSL SFLNSMQQNTG ANNIVATTQN GYKPGDLVSY QINDDGTVVG 300
NYSNEQTQLL GQIVLANFAN NEGLASEGDN VWSATQSSGV ALLGTAGTGN FGTLTNGALE 360
25 ASNVDLSKEL VNMIVAQRNY QSNAQTIKTQ DQILNTLVNL R 401

<212> Type : PRT
<211> Length : 401
SequenceName : SEQ ID 66
SequenceDescription :

30 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
35 MSKSTFLHIL ISSIILVALI QSSAWANCTN TQIGQTEDGR TALIEFGKIN MTDITYFAPAG 60
SLLATTVVPP TNYTSGGATG SSVLWECDAT DLPNIYFLVA TNGDDRVGGF YDAGGPDGLS 120
DVYATWFAFV GLKQTMAGVT LGRYWKKVPI TSYATQGTKI QIRLQDIPPL HAELYRISTL 180
PDTSATTSWC GNNNTDSSGV GFAKPSGTIY NCVQPNAYIQ LSGTSGILFG HDEPGEDSSV 240
HWDFWGADNG FGYGMRANR LYNNATCVAR SATPLVLLPT IAEAQLNAGM ESTGNFNVRV 300
40 ECSNSVQSGI SDTQTALGIQ VSEGAYTAAQ KLGINSNGG VSALVSDNYD AAEMAKGVGI 360
YISNSAHPDT AMTLVGQPGI AKLTPGGNAA GWYPVFEGAT LEGATHPGYS SYSYSFIARL 420
KKLPNQTVSA GKVRATAYIL VKMQ 444

<212> Type : PRT
<211> Length : 444
SequenceName : SEQ ID 67
SequenceDescription :

45 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MENNRRNFPAR QFHSITFFAG LCIGITPVAQ ALAAEGQTNA DDTLVVEAST PSLYAPQOSA 60
DPKFSRPVAD TTRTMTVISE QVIKQDQATN LTDALKNVPG VGAFVAGENG NSTTGDAIYM 120
RGADTSNSIY IDGIRDIGSV SRDTFNTEQV EVIKGPSGTD YGRSAPTGSI NMISKQPRND 180
55 SGIDASASIG SAWFRRTLD VNQVIGDTTA VRLNVMEKKT HDAGRDKVKN ERYGVAPSIA 240
FGLGTANRLY LNYLHVTQHN TPDGGIPTIG LPGYSAAPSAG TATLNHSGKV DTHNFYGTDS 300
DYDDSTTDTA TMRFEHDIND NTTIRNTTRW SRVKQDYLMT AIMGCASNIT QPTSDVNSWT 360
WSRTANTKDV SNKILTNQTN LTSTFYTASI GHVSTGVEF TRETQTNNGV NPVTLPVANI 420
YHPDSSIHPG GLTRNGANAN GQTDTFIYA FDTLQITRDF ELNGGIRLDN YHTBYDSATA 480
60 CGGSGRGAIT CPAGVAKGSP VTTVDTAKEG NLVNWKAGAL YHLTENGNGV INYAVSQPPP 540
GGNNFALAQS GSGNSANRTD FKPQKANTSE IGTKWQVLDK RLLLTAAALFR TDIENEVEQN 600
DDGTYSQYQK KRVEGYEISV AGNITPAWQV IGGYTQKAT IKNGKDVAQD GSSSLPYTPE 660
HAFTLWSQYQ ATDDISVGAG ARYIGSMHKG SDGAVGTPAF TEGYWVADAK LGYRVNRNLD 720
FQLNVYNLFD TDYVASINKS GYRYHPGEPR TFLLTANMHF 760

65 <212> Type : PRT
<211> Length : 760
SequenceName : SEQ ID 68

SequenceDescription :

Sequence

5 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MQMKLLLPIL IGLSLSGFSS LSQAENLMQV YQCARLSNPE LRKSAADRDA AFEKINEARS 60
PLLPQLGLGA DYTYSNGYRD ANGINSNATS ASLQLTQSIF DMSKWRALTL QEKAAGIQDV 120
TYQTDQQTLL LNTATAYFNV LNAIDVLSYT QAQKEAIYRQ LDQTTQRFNV GLVAITDVQN 180
10 ARAQYDTVLA NEVTARNNLD NAVEQLRQIT GNYYPELAAL NVENFKTDKP QPVNALLKEA 240
EKRNLSELLQA RLSQDLAREQ IRQAQDGHLP TLDLTASSGI SDTSYSGSKT RGAAGTQYDD 300
SNMGQNKVGL SFSLPYQGG MVNSQVKQAQ YNFVGASEQL ESAHRSVVQT VRSSFNNINA 360
SISSINAYKQ AVVSAQSSLD AMEAGYSVGT RTIVDVLDAT TTLYNKQEL ANARYNYLIN 420
QLNIKSALGT LNEQDLLALN NALSKPVSTN PENVAPQTPE QNAIADGYAP DSEAPVWQQT 480
15 SARTTTSNHG NPFRRN 495
<212> Type : PRT
<211> Length : 495
SequenceName : SEQ ID 69
SequenceDescription :
20 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
25 MTKLKLALG VLIATSAGVA HAEGKFSLGA GVGVEHPYK DYDDEVYPVP VINYEGDNFW 60
FRGLGGGYLL WNDATDKLSI TAYWSPLYFK AKDSGDHMR HLDDRKSTMM AGLSYAHFTQ 120
YGYLRTTLAG DTLDNSNGIV WDMAWLYRYT NGGLTVTPGI GVQWNSQNQN EYYYGVSRKE 180
SARSGLRGYN SNDSWSPYLE LSASYNFLGD WSVYGTARYT RLSDEVTDSP IVDKSWTGLI 240
STGITYKF 248
30 <212> Type : PRT
<211> Length : 248
SequenceName : SEQ ID 70
SequenceDescription :
35 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
40 MKKTLAAGA VLALSSSFTV NAAENDKPQY LSDWWHQSVN VVGSYHTRFG PQIRNDTYLE 60
YEAFAKKDWF DFYGYADAPV FFGGNSDAKG IWNHGSPLFM EIEPRFSIDK LTNTDLSFGP 120
FKEWYFANNY IYDMGRNKDG RQSTWYMLG TDIDTGLPMS LSMNVYAKYQ WQNYGAANEN 180
EWDGYRFBKIK YFVPITDLWG GQLSYIGFTN FDWGSDLGDD SGNAINGIKT RTNNSIASSH 240
ILALNYDHHW YSVVARYWHD GGQWNDDAEL NFGNGNFNVN STGWGGYLVV GYNF 294
45 <212> Type : PRT
<211> Length : 294
SequenceName : SEQ ID 71
SequenceDescription :
50 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
55 MLSTQFNDRN QYQAITKPSL LAGCIALALL PSAAFAAPAT EETVIVEGSA TAPDDGENDY 60
SVTSTSAGTK MQMTQRDIPQ SVTIVSQORM EDQQLQTLGE VMENTLGISK SQADSDRALY 120
YSRGFQIDNY MVDGIPTYFE SRWNLGDAIS DMALFERVEV VRGATGLMTG TGNPSAAINM 180
VRKHATSREF KGDVSAEYGS WNKERYVADL QSPLTEDGKI RARIVGGYQN NDSWLDYNS 240
EKTFFSGIVD ADLGDLTLS AGYEYQRIDV NSPTWGGLPR WNTDGSSNSY DRARSTAPDW 300
AYNDKEINKV FMTLKQRFAD TWQATLNATH SEVEFDSKMM YVDAYVNKAD GMLVGPYSNY 360
60 GPGFDYVGGT GWNNGKRKVD ALDLFADGSY ELFGRRHNLN FGGSYSKQNN RYFSSWANIF 420
PDEIGSFYNF NGNFPQTDWS PQSLAQDDTT HMKSLYAATR VTLADPLHLI LGARYTNWRV 480
DTLTYSMEKN HTTPYAGLVF DINDNWSTYA SYTSIFQPQN DRDSSGKYLA PITGNNYELG 540
LKSDDWMSRL TTTLAIFRIE QDNVAQSTGT PIPGSNGETA YKAVDGTVSK GVEFELNGAI 600
TDNQWLTFGA TRYIAEDNEG NAVNPNLPRT TVKMFTSYRL PVMPELTVGG GVNWQNRVYT 660
65 DTVTPYGTFR AEQGSYALVD LFTRYQVTKN FSLQGNVNNL FDKTYDTNVE GSIVYGAPRN 720
FSITGTYQF 729
<212> Type : PRT

<211> Length : 729
SequenceName : SEQ ID 72
SequenceDescription :

5 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MARFQFKNRK NNGLIFFISF MVMGEAAIAA PLPQWANAPA VTPVAQLSLQ ESILRAFARN 60
10 PGVTQQAQAI GIGEAQIDEA KSAWYPHVGL TGNAGPSRQT DSSGRLDNNV SYGITLTQLV 120
YDFGKTNDI NLQTAARDSY RFKLMATLTD VAEKTATAYM EVSRYQALCD AAQRNIHSLE 180
NVYNMAALRA NAGLNSSSDE LQAQTRIAGM RSTLEQYQAA MASAKAQLAV LTGVQPEAIA 240
APPAELAEQPV VSLKNIDYQS IPLVLAAENL RQSAQYGVK TKAQYWPTLS IQGGKTRYQT 300
SDRSYWDDQL QLVNVNAPLYQ GGAVSAQVQQ AEGQQKISAS QVEQAKLDVL QRASVAYANW 360
15 TGARGREEAG LAQSESAHKT RDVYQNEYKL GKRSNLNLLT VEQDVFQAQS AEINANYDGW 420
VAAVNYAAAV NNLIPLAGIK QGLYNLPLDL K 451
<212> Type : PRT
<211> Length : 451
SequenceName : SEQ ID 73
SequenceDescription :

20 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MAKFTSPFSG IKGRALFSLI FAAPMIHATD TATTKDGETI TVTADANTAT EATDGYQPLS 60
TSTATLTDMPL MLDIPQVVNT VSDQVLENQN ATTLEALYN VSNVQNTNL GGTQDAFVRR 120
GFGANRDGSI MTNGLRVTLP RSFNAATERV EVLKGPA STL YGILDPGGLI NVVTKRPEKT 180
FHGSVSATSS SFGGGTGQLD ITGPIEGTQL AYRLTGEVQD EDYWRNFGKE RSTFIAPSLT 240
30 WFGDNATVTM LYSHRDYKTP FDRGTIFDLT TKQPVNVDRK IRFDEPFNIT DGQSDLAQLN 300
AEYHLNSQWT ARFDYSYSQD KYSDNQARVT AYDATTGTLT RRV DATQGST QRMHSTRADL 360
QGNVDIAGFY NEILGGVSYE YYDLLRTDMI RCKNAKDFNI YNPVYGN TSK CTTVSASDSD 420
QTIKQESYSA YAQDALYLTDL NWIAVAGIRY QYYTQYAGKG RPFNVNTDSR DEQWTPKLGL 480
VYKLTSPSVSL FANYSQTFMP QSSIASYIGD LPPESSNAYE VGAKFELEFDG ITADIALFDI 540
35 HKRNVLYTES IGETIAKTA GRVRSRGVEV DLAGALTENI NIIASVGYTD AKVLEDPDYA 600
GKPLPNVPRH TGSFLTYDI HNMGPNNLT FGGGHCVSR RSATNGADYY LPGYFVADAF 660
AAYKMKLQYP VTLQLNVKNL FDKTYTSSI ATNNLGNQIG DPREVQFTVK MEF 713
<212> Type : PRT
40 <211> Length : 713
SequenceName : SEQ ID 74
SequenceDescription :

Sequence

45 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRTLQGWLLP VFMLPMAVYA QEATVKEVHD APAVRGSIIA NMLQEHDNPF TLYPYDTNYL 60
IYTQTSDLNK EAIASDWAE NARKDEVKFQ LSLAFPLWRG ILGPN SVLGA SYTQKSWWQL 120
50 SNSEESSPFR ETNYEPQLFL GFATDYRFAG WTLRDVEMGY NHDSNGRSDP TSRSWNRLYT 180
RLMAENGWNL VEVKPYVVG NTDDNPDIK YMGYYQLKIG YHLGDAVLSA KGQYNWNTGY 240
GGAELGLSYP ITHKVRLYTQ VYSGYGESLI DYNFNQTRVG VGVMLNDLF 289
<212> Type : PRT
<211> Length : 289
55 SequenceName : SEQ ID 75
SequenceDescription :

Sequence

60 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MAVQKNVIK ILAGTFALML SGCVTVPDAI KGSSPTPQQD LVRVMSAPQL YVGQEARFGG 60
KVVAVQNQQG KTRLEIATVP LDGARPTLG EPSRGRIYAD VNGFLDPVDF RGQLVTVVGP 120
ITGAVDGKIG NTPYKFMVMQ ATGYKRWHLT QQVIMPPQPI DPWFYGGRGW PYGHGGWGWY 180
65 NPGPARVQTV VTE 193
<212> Type : PRT
<211> Length : 193

SequenceName : SEQ ID 76
SequenceDescription :

5 Sequence

 <213> OrganismName : Escherichia coli O157:H7
 <400> PreSequenceString :
MRKQWLGICI AAGMLAActs DDGQQQT VSV PQPAVCNGPI VEISGADPRF EPLNATANQD 60
YQRDGKSYKI VQDPSRFIQA GLAAIYDAEP GSNLTASGEA FDPTQLTAAH PTLPIPSYAR 120
10 ITNLANGRMI VVRINDRGPY GNDRVISLSR AAADRLNTSN NTKVRIDPII VAQDGSLSGP 180
GMACTTVAKQ TYALPAPPDL SGGAGTSSVS GPQGDILPVS NSTLKSEDPT GAPVTSSGFL 240
GAPTTLAPGV LEGSEPTPAP QPVVTAPSTT PATSPAMVTP QAASQSASGN FMVQVGAVSD 300
QARAQQYQQQ LGQKFGVPGR VTONGAVWRI QLGPFANKAE ASTLQQRLQT EAQLQSFITT 360
AQ 362

15 <212> Type : PRT
 <211> Length : 362
 SequenceName : SEQ ID 77
 SequenceDescription :

20 Sequence

 <213> OrganismName : Escherichia coli O157:H7
 <400> PreSequenceString :
MIKRVLVISM VGLSLVGCVN NDTLSGDVYT ASEAKQVQNV SYGTIVNVRP VQIQGGDDSN 60
25 VIGAIGGAVL GGFLGNTVGG GTGRSLATAA GAVAGGVAGQ GVQSAMNKTQ GVELEIRKDD 120
GNTIMVVQKQ GNTRFSPGQR VVLASNGSQV TVSPR 155
 <212> Type : PRT
 <211> Length : 155
 SequenceName : SEQ ID 78
30 SequenceDescription :

 Sequence

 <213> OrganismName : Escherichia coli O157:H7
35 <400> PreSequenceString :
MSKATEQN DK LKRAIIISAV LHVILFAALI WSSF DENIEA SAGGGGGSSI DAVMVD SGAV 60
VEQYKRMQSQ ESSAKRSDEQ RKMKEQQAEE ELREKQAEEQ ERLKQLEKER LAAQE QKKQA 120
EEAAKQAE LK QKQAE EAAK AAADAKAKAE ADDKAAEEAA KKAADAKKK AEAEAAKAAA 180
EAQKKA EAAA AALKKKA EAA EAAAEARKK AA AEKAAADK KAAEKAAAEK AAADKKAAAE 240
40 KAAADKKAAA AKAAAEKAAA AKAAAEADDI FGELSSGKNA PKTGGGAKGN NASPAGSGNT 300
KNNGASGADI NNYAGQIKSA IESKFYDASS YAGKTCTLRI KLAPDGM LLD IKPEGGDPAL 360
CQAALAAAKL AKIPKPPSQA VYEVFKNAPL DFKP 394
 <212> Type : PRT
 <211> Length : 394
45 SequenceName : SEQ ID 79
 SequenceDescription :

 Sequence

50 <213> OrganismName : Escherichia coli O157:H7
 <400> PreSequenceString :
MMKFKKCLLP VAMLASFTLA GCQSNADDHA ADVYQTDQLN TKQETKTVNI ISILPAKVAV 60
DNSQNKRNAI AFGAMNIGAVA GGVIGHNVGS GSNSTGTAGA VGGGAVGAAA GSMVNDKTLV 120
EGVSLTYKEG TKVYTSTQVG KECQFTTGLA VVITTTYN ET RIQPNTKCPE KS 172
55 <212> Type : PRT
 <211> Length : 172
 SequenceName : SEQ ID 80
 SequenceDescription :

60 Sequence

 <213> OrganismName : Escherichia coli O157:H7
 <400> PreSequenceString :
65 MLLSIITVAF RNLEGIVKTH ASLAHLAQAE DISFEWIVVD GGSNDGTREY LENLNGIYNL 60
RFVSEPDNGI YDAMNKGIAM AQGKFALFLN SGDIFHQDAA YFVRKLKMQK DNVMITGDAL 120
LDFGDGHKIK RSAKPGWYIY HSLPASHQAI FFPVSGLKKW RYDLEYKVSS DYALAAKMYK 180

AGYAFKKLNG LVSEFSMGGV STTNMELCA DAKKVQRQIL HVPGFWAELS WHLRQRTTSK 240
TKALYNKS 248
<212> Type : PRT
<211> Length : 248
5 SequenceName : SEQ ID 81
SequenceDescription :

Sequence

10 <213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MKLTTLQTLK KGFTLIELMI VIAIIAILAT IAIPSYQNYT KKAASSELLQ ASAPYKADVE 60
LCVYSTNETT SCTGGKNGIA ADIKTAGGYV ASVITQSGGI TVKNGTLAN MEYILQAKGN 120
AAAGVTWTTT CKGTDASLFP ANFCGSVTK 149
15 <212> Type : PRT
<211> Length : 149
SequenceName : SEQ ID 82
SequenceDescription :

20 Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
25 MLNKKFKLNF IALTVAAYALT PYTEAALVRD DVDYQIFRDF AENKGRFSVG ATNVEVRDKN 60
NHS LGNVLPN GIPMIDFSV DDKRIATLI NPQYVVGK V SNGVSELHF GNLNGNMNNG 120
NAKSHRDVSS EENRYFSVEK NEYPTKLNGK AVTTEDQTQK RREDYYMPRL DKFVTEVAPI 180
EASTASSDAG TYNDQNKYPA FVRLGSGSQF IYKKGDNYSL ILNNHEVGGN NLKLVGDAYT 240
YGIAGTPYKV NHENGLIGF GNSKEEHS DP KGILSQDPLT NYAVLGDSGS PLFVYDREKG 300
KWLFLGSYDF WAGYNKKSQ EWN IYKPEFA KTVLDKDTAG SLTGSNTQYN WNPTGKTSVI 360
30 SNGSESLNVD LFDSSQD TDS KKNNHGKSVT LRGSGLTLTN NNIDQGAGGL FFEGDYEVKG 420
TSDSTTWKGA GVSVDGKTV TWKVHNP KSD RLAKIGKGT L IVEGKGENKG SLKVG DGTVI 480
LKQADANNK VKAFSQVGIV SGRSTVVLND DKQVDPNSIY FGFRGGR L DA NGNNLT FEHI 540
RNIDDGARLV NHNTSKTSTV TITGESLITD PNTITPYNID APDEDNPYAF RRIKDG GQLY 600
LNLENYTYYA LRKGASTRSE LPKNSGESNE NWLYMGKTS D EAKRNV MNHI NNERMNGFNG 660
35 YFGE EEGKNN GN LNVTFKGK SEQNRFL LTG GTNLNGDLKV EKGTLFLSGR PTPHARDIAG 720
ISSTKKDQHF AENNEVVVED DWINRNFKAT NINVTNNATL YSGRNVANIT SNITASD NAK 780
VHIGYKAGDT VCVRS DYTGY VTCTTDKLS D KALNSFNATN VSGNVNLSGN ANFVLGKANL 840
FGTISGTGNS QVRLTENS HW HLTGDSNVNQ LNLDKGHIHL NAQNDANKVT TYNTLT VNSL 900
SGNGSFYILT DLSNQGD KV VVTKSATGNF TLQVADKTGE PTKNELTLFD ASNATRN LNLN 960
40 VSLVGNTVDL GAWKYKLRNV NGRYDLYNPE VEKRNQTVDT TNITTPNNIQ ADVPSVPSNN 1020
EELARVETPV PPPAPATPSE TTETVAENSK QESKTVEKNE QDATETT AQN GEVAEEAKPS 1080
VKANTQTNEV AQSGSETEET QTTEIKETAK VEKEEKAKVE KDEIQEAPQM ASETSPKQAK 1140
PAPKEVSTDT KVEETQVQAQ PQTQSTTVAA AEATSPNSKP AEETQPSEKT NAEPVTPVVS 1200
KNQTENTTDQ PTEREKTAKV ETEKTQEP PQ VASQASPKQE QSETVQPQAV LESENVP TVN 1260
45 NAEEVQAQLQ TQTSATVSTK QPAPENSINT GSATAITETA EKSDKPQTET AASTEDASQH 1320
KANTVADNSV ANNSESSDPK SRRRRSISQP QETSAEETTA ASTDETTIAD NSKRSKPNRR 1380
SRRSVRSEPT VTNGSDRSTV ALRDLTSTNT NAVISDAMAK AQFVALNVGK AVSQHISQLE 1440
MNNEGQYNVW VSNTSMNENY SSSQYRRFSS KSTQTQLGWD QTISNNVQLG GVFTYVRNSN 1500
NFDKASSKNT LAQVNFYSKY YADNHWYLG I DLGYGKFQSN LKTNHNAKFA RHTAQFGLTA 1560
50 GKAFNLGNFG ITPIVGV RYS YLSNANFALA KDRIKVPIS VKTAF AQVDL SYTYHLGEFS 1620
VTPILSARYD TNQSGSKINV NQYDFAYNVE NQQQYNAGLK LKYHNVKLSL IGGLTKAKQA 1680
EKQKTAELKL SFSF 1694
<212> Type : PRT
<211> Length : 1694
55 SequenceName : SEQ ID 83
SequenceDescription :

Sequence

60 <213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MALVNKIKTL SSVGILAATL FLAGCQAQSN ILAFTPPAPS ASMNVNRTAV VSVTTKDSRA 60
IQEIASYTKH GELIKLNASP SVTQLFQQVM QQNLI SKGFR VGQLNGSNAW VTVDVREFGT 120
QVEQGNLRYK LNTKIQATVY VQGA KGSYNK SFNVTHSQEG VFNAGNDEIH KVLSTQTFNDI 180
65 VNNIYQDQEV AA AINQYSN 199
<212> Type : PRT
<211> Length : 199

SequenceName : SEQ ID 84
SequenceDescription :

Sequence

5 -----
<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MLCWIGYKNG ILPQQNSTLY PWNPSKCGV IFDGFQLVGD DFNSDQTAEN TSPAQVQLYT 60
THLQSCSPIH SGENFAPIPL YKQLKNQPHL SQDLIKWQEN WQACDQLQMN GAVLEQQSLA 120
10 EISDHQSTLS KHGRYLAQEI EKETGIPTY YLYRVGGQSL ESEKSRCCPS CGANWALKDA 180
IFDTFHFKCD TCRLVSNLSW NFL 203
<212> Type : PRT
<211> Length : 203
SequenceName : SEQ ID 85
15 SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
20 <400> PreSequenceString :
MGAFAFASVT NANIYAEGDI GLSQTKANGS NNTRVGPRVS VGYKVGNTRV AGDYTHHGKV 60
DGTKIQGLGA SVLYDFDTNS KVQPYVGARV ATNQFKYTNR AEQKFKSSSD IKLGYGVVAG 120
AKYKLDGNWY ANGGVEYNRL GNFDSTKVNN YGAKVGVGYG F 161
<212> Type : PRT
25 <211> Length : 161
SequenceName : SEQ ID 86
SequenceDescription :

Sequence

30 -----
<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MKKLLIASLL FGTTTTVFAA PFVAKDIRVD GVQGDLEQQI RASLPVRAGQ RVTDNDVANI 60
VRSLFVSGRF DDVKAHQEGD VLVVSVVAKS IISDVKIKGN SIIPTEALKQ NLDANGFKVG 120
35 DVLIREKLNE FAKSVKEHYA SVGRYNATVE PIVNTLPNNR AEILIQINED DKAKLASLTF 180
KGNESVSSST LQEQMELQPD SWWKLWGNKF EGAQFEKDLQ SIRDYYLNG YAKAQITKTD 240
VQLNDEKTKV NVTIDVNEGL QYDLRSARII GNLGMSAEL EPLLSALHLN DTFRRSDIAD 300
VENAIKAKLG ERGYGSATVN SVPDFDDANK TLAITLVVDA GRRLTVRQLR FEGNTVSADS 360
TLRQEMRQQE GTWYNSQLVE LGKIRLDRTG FFETVENRID PINGSNDEV VVYKVKERNT 420
40 GSINFGIGYG TESGISYQAS VKQDNFLGTG AAVSIAGTKN DYGTSVNLGY TEPYFTKDG 480
SLGGNVFFEN YDNSKSDTSS NYKRRTYGSN VTLGFPVNE NSYYVGLGHT YNKISNFALE 540
YNRNLYIQSM KFKGNGIKTN DDFDSFGWNY NSLNRGYFPT KGVKASLGGR VTIPGSDNKY 600
YKLSADVQGF YPLDRDHLWV VSAKASAGYA NGFGNKRLPF YQTYTAGGIG SLRGFAYGSI 660
GPNAIYAEHG NGNGTFKKIS SDVIGGNAIT TASAELIVPT PFVSDKSQNT VRTSLFVDAA 720
45 SVWNTKWKSD KSGLDNNVLK SLPDYGKSSR IRASTGVGFQ WQSPIGPLVF SYAKPIKKYE 780
NDDVEQFQFS IGGSF 795
<212> Type : PRT
<211> Length : 795
SequenceName : SEQ ID 87
50 SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
55 <400> PreSequenceString :
MLKKTSLIFT ALLMTGCVQN ANVTTPQAQK MQVEKVDKAL QKGEADRYLC QDDRVRVVRVH 60
ATHKKYKKNL HYVTVTFOGV SEKLTLMISE RGKNYANIRW MWQERDDFST LKTNLGEILA 120
TQCVSQTSE LSGQ 134
<212> Type : PRT
60 <211> Length : 134
SequenceName : SEQ ID 88
SequenceDescription :

Sequence

65 -----
<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :

	MRIIIIFFMG	LNMNTNFRLER	ACLFYAWAN	GRCCLCSSTN	QPTNQPTNQPTN	TNQPTNQPTN	60
	QPTNQNSNVS	EQLEQINVSG	STENSDTKTP	PKIAETVKTA	KTLEREQANN	IKDIVKYETG	120
	VTVVEAGRFG	QSGFAIRGVD	ENRVAINIDG	LRQAETLSSQ	GFKELFEGYG	NFNNTRNGAE	180
	IETLKEVNIT	KGADSIKNGS	GSLGGSVIYK	TKDARDYLIN	KDYVVSYYKG	YATENNQSFD	240
5	TLTLAGRYKK	FDDLVTTSR	NGHELENYGY	KNYNDKIQGG	KREKADPYKI	EQDSTLLKLS	300
	FNPTENHRFT	FAADLYEHRS	RGQDLSYTLK	YQRCNETPE	VDSRHTNDKT	KRRNISFSYE	360
	NFSQTPFWD	LKLTYSQDRI	KTRARTDEYC	DAGVRHCEGT	DNPTGLKVTN	GKITRRDGS	420
	LQFEEKNNTA	KSSDKTYDFK	KFIDTDKRV	DDKLVLNNPS	DTWYDCSIFN	CENNAKIKVF	480
	KGNYYGYDG	KWKEVDLEIK	ELNGKKFAKI	KDNDRIKISI	LPSSPGYLER	LWQERDLDTN	540
10	TQQLNLDLTK	DFKIWHIEHN	LQYGGSYNTA	MKRMVNRAGN	DASDVQWWAT	PTLGEDSWTG	600
	KPHTCATTYE	WNANLCPRVD	PEFSYLLPIK	TTGKSVYLF	NFVITDYLSF	DLGYRYDNIH	660
	YQPKYKHGIT	PKLPDDIVKG	LFIPLPNNSN	SDPNKVKENV	QQNIDYIAKQ	NKKYKAHSYS	720
	FVSTIDPTSF	LRLQLKYSKG	FRTPTSDEMY	FTFKHPDFTI	LPNTDLKPEI	AKTKETIAFTL	780
	HNDDWGFIST	SLFKTMYKNF	IDLIFKKQET	FVGGSGRGE	TLFFSLYQNI	NRDNASLKG	840
15	EINSKVFGLK	MAKPMDFNL	SYKYTYQGR	MNGNIPMNAI	QPRTMVYGLG	YDHPNHKFGF	900
	DFYTTTHVASK	NPEDTYNMFY	KEENKKDSTI	KWRSKSYTIL	DLIGYVQPIK	NLTIRAGVYN	960
	LITNRKYITWD	SARSIRSGT	SNVIDQSTGL	GINRFYAPGR	NYKMSVQFEF		1010
	<212> Type : PRT						
	<211> Length : 1010						
20	SequenceName : SEQ ID 89						
	SequenceDescription :						
	Sequence						

25	<213> OrganismName : Helicobacter pylori J99						
	<400> PreSequenceString :						
	MTYRNGKIDL	KERFSKNRSF	KGIKKKIACK	YTIKNSLSII	YSLKTHSNSS	LSINKKIFLG	60
	LGFVSALSAQ	SEDYNSSVYV	LNSVNNNNNN	KSYIISPLRT	WAGGNRSFTQ	NYNNSQLYIG	120
	TKNASATPNH	SSVWFGEKGY	IGFITGVFKA	RDIFITGAVG	SGNELKTGGG	AILVFESSNE	180
30	LTTNGAYFQN	NRAGTQTSWI	NLISNNSVNL	TNTDFGNQTP	NGGFNVMGK	ITYNGGSGVNG	240
	GNFGFDNVDS	NGATTISGVT	FMNNGALTYK	GGNGTGGSI	FTNSNINHYK	LNLNANSVTF	300
	NNSTLGSMPN	GNNATIGNAY	ILNANNITFN	NLTFNGGWV	PNRSDAHVNF	QGTITINNPT	360
	SPFVNMTGKV	TINPNAIFNI	QNYTPTIGNA	YTLFKNKNGN	IAYDDVNNLW	NIIRLKNTQA	420
	TKDNKSNATS	NNNTHTYVY	YNLGGTLYHF	RQIFSPDSIV	LQSVYYGANN	LYYTNSVNIH	480
35	DNVFNKLNIN	DDRADTIFYL	NGLNTWNTYQ	ARFAQTYGGK	NSALVFNAAT	PWANGAIPKS	540
	NSTVRFGGYE	GVNWGKTGYI	TGTFADRVY	ITGNMMSGNG	AQTGGGATLN	FVGATEINIA	600
	GATFKNLKT	SQNSYMTFMA	LGNNGSGSKI	NVSQSDFYDW	TDGGYDFTCN	GVFDSVNFNK	660
	AYYKFQGAEN	SYNFKNTNFI	AGNFKFQGKT	TIEKSVLND	SYAFDGVNNA	FNEDKFNNGS	720
	FNFNHAQTN	AFNNNSFSGG	SFSFNAKQVD	FNGNSFNGGV	FNFNNTPKAS	FTNDTFNVNN	780
40	QFKINGAQT	FTFSKGVVFN	MQGLLSLSLV	GTTYQLLNK	SVGYKDNNA	LYQMLRWTSG	840
	ENPSGKLVD	NKTPNFAKI	YNVQFTDNG	YTYIKENFNN	GITLTRLCTL	GYTHCVNIDN	900
	DAFNLKNVNN	NASNTVFYLN	GMTTWKTAGT	GVFTQDYS	NSVLVFNQTT	PFLAGANPTS	960
	NSVVGFGKTS	GAEWGLVGYI	QGVFKANQID	ITGTIRSGNG	AKTGGGATLV	FNAQERLNIA	1020
	NANLNNDKAG	LQNSWMNFIV	NNGNLNVINA	NFSNQTPHGG	FNKANNITW	DKGSVSGGGN	1080
45	FGVDNANANG	NAVINKNVNF	DNGTLIYKGG	ENSAGNSLTL	ENNTFNNSYNI	NAKAQNLIFN	1140
	NNSFNNGSYS	FNDTKNVTFK	GTNTLINSDF	FSRLKGSVSI	DNNSIFNIE	DLTDKTTYTL	1200
	LSGDNIKYYN	QALADNVFSK	NLWDLIHYDG	EQGTLRLTDN	NTYFVQFTQS	NGQKFVFEET	1260
	FNPGSITYKY	FTIHSSPFHT	EADSKDIWNQ	VRKQDFDIPG	KTPVCVGVCY	IAPYKNQDLI	1320
	GSSAFAWSLN	FGATVVGTL	LGSAQEKANN	NGGSIWFGKN	NLLYLHGNFN	ATNIFLTNNF	1380
50	NVGNPNAGGG	ATINFNADET	LSADGLNYTN	FQTVAMGLQT	SASQHSWANF	NSKLSMEIKN	1440
	SNFRDFTWGG	FRFNSGRITF	ENTTFSGWTN	INGATESGSS	VNMVANTDL	IFTDSLGGG	1500
	IRYDLKANNI	IFNNTQMVD	VSKNVNQSSL	NGNVTFNHSR	LSVKPNAAIN	IGGDQTTQTL	1560
	ENASSLSFYN	DSVANFNQTT	AFNGVSYLNL	NPNAQVSFNG	ANFNANVTF	YGIPLFGKTP	1620
	NFGNSVRLIN	FKGDAKFNA	TLNLRAKNIH	LNFQGAFTFE	NNSTMNLAES	SQASFNALS	1680
55	EGETNFNLNG	SSLLSFNGNS	VFNAPVNFYA	NNSQISFTHS	ATFNADASFD	LGNNSTLNQ	1740
	SVLLNSALNL	LGNGGNNLAI	NAKGNFSFGS	QGILNLSYMN	LFGGDKKASV	YDVLQAQNI	1800
	GLRGNGGYEK	IRFYGIQIEK	ADYSFNNGVH	SWSFTNPLNT	TETITETLHN	NRLKVQISQN	1860
	GASNNAMFNL	APSLYDYQQN	PYDESENSYN	HTSDKAGTY	LSSSIKGF	NNEIPGTYNA	1920
	QNQPLQALHI	YNQAIQKQDL	NMIASLGKEF	LPKVAKLIAS	GALDNLNLNS	PDSFETIFSI	1980
60	LKEYGITLNG	ANWKSLLKII	NNFSNTANYH	FSQGSIVVGA	IKEGQNTNNS	VVWFGGDGYK	2040
	NPCAVGDNTC	QMFRQTNLQ	LLNSSVPLG	YINANFKAKN	YITGTIGSG	NAWGSGGSAN	2100
	VSFESATNLV	LNQANIDAQ	TDKIFSYLKG	EGIDKLFGEK	GLGNVLSNIV	YEESLNDNAI	2160
	PKDLANMIPK	DLGSKTSLSS	LSPTENVNLL	GVSAFKNAIM	EILNSKTVD	VFGENGLLNA	2220
	LDPVKRKEID	QMLLEQIQAH	SSGFEKFIVK	TLGIENVENF	INNWWYKQSL	SSFANFVPG	2280
65	GLNQALDKIG	SSDAKDLQS	FLDKTTFGDI	LNQMINQAPL	INKLISWLGP	QDLSVLVNI	2340
	LNSITNPSKE	LLGAISGMGQ	KVLNDLLGEG	VVNKIMSNQV	LGQMINKIIA	DKGFGGVYHQ	2400
	GLGSILPKSL	QDELKKLG	SLKPKGLHN	LWQKGNFNFV	AKNHVFNNS	LFSNATGGEL	2460

	NFVAGKSIIF	NGKNTINFQT	YQGRLSFVSK	DFSNISLDTL	NATNGLTLNA	SKNDISVQKG	2520
	QICVNVLDQM	TAKGKTTQTN	SSSSATAPTN	ETLEVSANNF	AFLGTIKANG	LVDFSQVLQN	2580
	TTIGTLDLGP	NATFKANNLI	VNNAFNNSN	YRANISGNFN	VAKGATFSTN	ENGLNVGGNF	2640
	NSEGPLIFNL	NNPTHQTIIN	VTGTSTIMSY	NNQALINFNT	QLKQGAYTLI	NANRMVGYD	2700
5	NQTILGGSLS	DYKLYTLID	FNGKRMQLNG	DSLSDNQPV	SIKDGGLVVS	FKDNQGMVY	2760
	SSILYDKIQV	TVSDKPMISQ	APSLEYVVKR	IQGSAGLNAI	KSAGNNSIMW	LSELFAAKGG	2820
	NPLFAPYYLQ	DNPTEHIVTL	MKDITSALGM	LSNSNLKNNS	TDVLQLNTYT	QMSRLAKLS	2880
	NFASFSDTDF	SERLSSSLKNQ	RFADAVPNAM	DVILKYSQRD	KLKNLWATG	VGGVSFVENG	2940
	TGTLYGVMVG	DYDFVRGVIV	GGYAAAGYSG	FYERITSSKS	DNVDVGLYAR	AFIKKSELTF	3000
10	SVNETWGANK	TQISSNDALL	SMINQSYKYS	TWTTNAKVNY	GYDFMFKNKS	IILKPQIGLR	3060
	YYYIGMSGLE	GVMNVLYNQ	FKANADPSKK	SVLTIDFALE	NRHYFNTNSY	FYAIGGVGRD	3120
	LLVNSMGDKL	VRFIGNNTLS	YRKGDLYNTF	ANITTGGEVR	LFKSFYANAG	VGARFGLDYK	3180
	MIDIIGNIGM	RLAF					3194

<212> Type : PRT
 15 <211> Length : 3194
 SequenceName : SEQ ID 90
 SequenceDescription :

Sequence

 20 <213> OrganismName : Helicobacter pylori J99
 <400> PreSequenceString :
 MKQFKKKPKK IKRSHQNQKT ILKRPLWLMP LLIIGGFASGV YADGTDILGL SWGEKSQKVC 60
 VHRPWYAIWS CDKWEKTTQQ FTGNQLITKT WAGGNAANY YHSQNNQDITA NLKNDNGTYF 120
 25 LSGLYNYTGG EYINGGNLDIE LGSNATFNLG ASSGNSFTSW YPNGHTDVTF SAGTINVNNS 180
 VEVGNRVGSG AGTHTGTATL NLNANKVTIN SNISAYKTSQ VNVGNANSVI TINSVSLNGD 240
 TCSSLARVGV GANCSTSGPS YSFKGTTNAT NTFNSSSGS FTFEENATFS GAKLNGGAFT 300
 FNKKFNATNN TAFNSGSFTF KGTSSFNAN FSNASYTFNN QATFQNSSFN GGTFTFNDQT 360
 NQSTQHPQIQ NSSFSGSATT LKGFATFEQA FNNSNHQLTI QNASFNNAFT NNTGKITIEK 420
 30 DASFNNTSFN TPVDTNMTI SGGVTLGSKN DLKNGATLDF GSKITLTQG TTFNLTLGSL 480
 EKSVTILNSR GGITYNHLLN HAINSLTNAL KTNESSEKPK SPAQGLWDMI TYNGVTGQLL 540
 NENAATSKPT DSSPSKSSTN STQVYQVGYK IGDITYKLQE TFSHNSIIIQ ALESGETYTPP 600
 PVINGSKFDL SASNYINADM PWYNHKKYIP KSNFTESGT YYLPSVQIWG SYTNSFKQTF 660
 SASNSNLVIG YNATWTDHNV SSSDTVAFGD TSGSALNGHC GPWPYYQCTG TTNGTYSAYH 720
 35 VYITANLRSG NRITGGAAN LIFNGVDSIN IANATTQHN AGAYSSSMTF STQNMDSQN 780
 LNGLNSNGKL LVYGTFTTNQ AKDNGFIFNA QATFENTNF NGGSYQFSGD SLNFSNNNQF 840
 NSGSFETGAK NTIFNNANFN NSTSFNFNNS SATTSFVGDF TNANSNLQIA GNAVFGNSTN 900
 GSQNTANFNN TGSVNAGNA TFDNVVFNSP TNSVKGKVT LNNITLKNLN APLSFGDGTI 960
 VFAHSVINI GEATNGNPI TLVSSSKAIE YNDAFSKNLW QLINYQGHGA SSEKLVSAG 1020
 40 NGVYDVVYF NNQTYNFQEV FSPNSISIRR LGVGMVFDYV DMEKSDRLYY QNALGFMITYM 1080
 PMSYNNLGN LNNITYYYDN SIDFYASGKT LFTKAEFSQT FTGQNSAIVF GAKNIWTSVS 1140
 DAPQSNVIR FGDNKGAGSN DASGHWCWNLQ CIGFITGHE AQKIYITGSI ESGNRISGG 1200
 GASLNFNLQ GILLTNATLY NRAAGTQSSS MNFVNSANI QAQNSYFIDD TAQNKGNPNF 1260
 SFNALNLDFS NSSFRGYVQG TQSVFKFNAV NAISFTNSSN LSSGLYQMQA KSVLFDNSNL 1320
 45 SVSVGTSSIK ANAINLSQNA SINASNHSTL ELQGDILNLD TSSLNLNQA INVSNNATIN 1380
 DYASLIASNG SHLNFNAGVN FNSANITSL SSSSIVFKA VSLRGQFNLS NNSLDFQGS 1440
 SAITSNTAFN FYDNAFSQSP ITFHQALDIK VPLSLGGLNL NPNSSSVLNL KNSQLVFSQD 1500
 GSLNIANIDL LSDLNGKNR VYNIQADMN GNWYERINFF GMRINDGIYD AKNQTYSFNT 1560
 PLNNALKITE SFKNNQLSVT LSQIPGIKNT LYNIGSEIFN YQKVYNNANG VYSYSDDAQG 1620
 50 VFYLTSSVKG YYPNPQSYQA SGSNNTTKNN NLTSESSVIS QTYNAQCNPI SALHVYNKGY 1680
 NFSNIKALGQ MALKLYPEIK KILGNDFSL SLSNLKGDAL NQLTKLITPS DWKNINELID 1740
 NANNVSVQNF NGTLLIGAT KIGQTDNTSA VVFGGLGYQK PCDYTDIVCQ KFRGTYLGQL 1800
 LESISADLGY IDTTFNAKEI YLTGTLGSGN AWGTGGSASV TFNSQTSLLI NQANIVSSQT 1860
 DGIFSMLGQE GINKVFNQAG LANILGEVAM QSINKAGGLG NLIVNTLGSD SVIGGYLTPE 1920
 55 QKNQTLSQLL GQNNFNDLMN DSGINTAIKD LIRQKLGFWT GLVGGLAGLG GIDLQNPKEK 1980
 IGMSINDLL SKKGLFNQIT GFISANDIGQ VISVMLQDIV KPSDALKNDV AALGKQMI 2040
 FLGQDTLNSL ESLLQNNQIK SVLDKVLAAK GLGSYEQGL GDLIPNLGKK GIFAPYGLSQ 2100
 VWQKGDFFSN AQGNVVFQNS TFSNANGGTL SFNAGNSLIF AGNNHIAFTN HSGTLNLLSN 2160
 QVSNINVTML NASNGLKINA TNNNVSVSQG NLFINASCQV QSDPTASAT NPCTTAQNA 2220
 60 SSSNASNNAP IALNNDES LVTANGFNFS GNIYANGVVD FSKIKGSANV KNLVLYNNAQ 2280
 FQANNLTISN QAVLEKNASF VTNNATQKIE VLQNLVIASN ASLSTGIYGL 2340
 EVGGALNNLG AIHFNLNSQ TPVNPLIQVG GIINLNTTQT PFMNVSVANG GTYTLKSSR 2400
 YIDYNINPNS LQSYLKYTL ININGNHIEE KNGVLTLYLQ RVLLQDKGLL LSVALPNSNN 2460
 ASQNNILSLS VLHNQIKMSY GNKVMDFTPP TLQDYIVGIQ GQSALNQIEA VGGNNAIKWL 2520
 65 STLMMETKEN PLFAPYILEN HSLNEILGVT KDLQNTASLI SNPNFRNNAT SLEMASYTQ 2580
 QTSRLTKLSD FRAREGESNF SERLLELKNK RFSDPNPSEV FVKYSQLSKH PNNLWIQGVG 2640
 GASFISGGNG TLYGLNVGYD RLVKSVILGG YVAYGYSGFN GNIMHSLANN VDVGMYARAF 2700

LKRNEFTLSA NETYGGNASH INSSNSLLSV LNQRNYNTW TTSVNGNYGY DFMFKQKSVV 2760
 LKPQVGLSYH FIGLSGMKGK MQNPAYQQFV MHSNPSNESV LTLNMGLESR KYFGKNSYYP 2820
 VTARLGRDLL IKAKGDNVVR FVGENTLLYR KGEIFNTFAS VITGGEMHLW RLMYVNAGVG 2880
 LKMGLQYQDL NITGNVGMVRV AF 2902

5 <212> Type : PRT
 <211> Length : 2902
 SequenceName : SEQ ID 91
 SequenceDescription :

10 Sequence

 <213> OrganismName : Helicobacter pylori J99
 <400> PreSequenceString :

15 MAFKKARLIS RFISKGSFKL NKISKKFFTL NQILKREKPI KRHKKTKSIE KPFNKNKSFL 60
 KASVLLIGAL GGLSHLRANE CRYWSWSSWS YQDNIESGPN SPTHNSYCLF SSAQGSSTYY 120
 LNTLTYSAG GASFTQKFNG GTLDIGGNIR FGGTGINGGD VGYITGTINA QTMNFNSSHI 180
 TTGNSYADGG GTTLNFNATN NITINQASFD NSDAGTQKSY MNFKGSNIKI SGSSFTDDTN 240
 GGFNFSGNNN NSTISFNQTS FNQGTYNFSN SATLSFNNSN FNQGTYHFNS AQSTFENSNF 300
 NQGTYNFNDN TSFNNDTFNQ GTYNFNSSKV SFSGANTLNS SSPFASLKGS VSFNSGAIFN 360
 20 LNQTNNNNQ YDILTTNGAI QYGVYQSYLW DLSQYQSGDKA ISHVEVSNNIT YDVTDFDINGQ 420
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 SNPTILKDAQ GLENTNQIQ QDEKALEKDL AQIKQLANST TGFNEQAFTQ AQKQEQQDEQ 540
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 NLVYVRNWNQ GWFKLQKTYN NKGIYYIDPN LSGQSGQSGN TLSTYTANLL GRSFGVNANN 660
 25 GTLIIGNNTE SVNDNGLIWI GHGGFGYITG TFSAAANIYLT NNFKTGEGVS NSDGGGANIT 720
 FKASDNITMD GLNYNNAETV TKMIQTGASQ HSYTTFDATN NISVTDSDFS DMTWGKFSFS 780
 AKNISFSNAS FSGFTNPGGG STISTNASNS LSFTDSRLNG GAIYNLQANS LIFNNTQAVF 840
 NVLYSRGTSN FNATTQLLGN TSFTLSSQSL LNFNGDTTLQ NNANITLGNK SQAFAKNSLT 900
 LDNNSNLSLD NQSVLNANGT SAFNNQASLN IYNGSQAAFS SLFFNGGTLN LNANSKLNAS 960
 30 SASFSNNTTI NLDDSVLNAN NTSSLNANIN FQGASQADFG GNTTIDTASF NFDSASSLNF 1020
 NNLTANGALN FNGYAPSLTK ALMNVSGQFV LGNNGDINLS DINIFDNITK SVTYNILNAQ 1080
 KGITISGAN GYEKILFYGM KIQNATYSDN NNIQTWSFIN PLNSSQIIQE SIKNGDLTIE 1140
 VLNNPNSASN TIFNIAPELY NYQDSKQNP GYSYDYSNQ AGTYYLTSNI KGLFTPKGSQ 1200
 TPQTPGTYSF FNQPLNSLNI YNKGFSSENL KTLGILSQN SATLKEMIES NQLDNITNIN 1260
 35 EVLQLLDKIK ITQAQKQALL ETINHLTDNI NQTFNNGNLV IGATQDNVTN STSSIWFEGN 1320
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 SADVTFQSAN NLVLNKANIE AQATDNIFNL LGQEGIDKIF NQGNLANVLS QMAMEKIKQA 1440
 GGLGNFIENA LSPLSKELPA SLQDETLGQL IGQNNLDDL NNSGVMNEIQ NIISQKLSIF 1500
 GNFVTPSIIE NYLAKQSLKS MLDDKGLLNF IGGYIDASEL SSILGVILKD ITNPPTSLOK 1560
 40 DIGVVANDLL NEFLGQDVVK KLESQGLVSN IINNVISQGG LSGVYNQGLG SVLPPSLQNA 1620
 LKENDLGTL SPRLGLHDFWQ KGYFNFLSNG YVFNNSFS NATGGSLNFV ANKSIIFNGD 1680
 NTIDFSKYQG ALIFASNGVS NINITTLNAT NGLSLNAGLN NVSVQKEIC INLANCPTTK 1740
 NSSPANSSVT PTNESLSVHA NNFTFLGTII SNGAIDLSQV TNNSVIGTLN LLENATLQAN 1800
 45 NLTTNAFNN ASNSTANIDG NFTLNQOATL STNASGLNVM GNFNYSYGLV FNLSHSVSHA 1860
 IINTQGTATI MANNNPLIQF NASSKEVGTY TLIDSAKAIY YGYNNQITGG SSLDNYLKLY 1920
 ALIDINGKHM VMTDNGLTYN GQAVSVKDG LVVGFKDSQN QYIYTSILYN KVKIIVSNDP 1980
 INNPAQPTLK QYIAQIQGVQ SVDSIDQAG NQAINWLNI FETKGSPLFA PYLLESHSTK 2040
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 ALKNKRFADA IPNAMDVILK YSQNRVKNV VWATGVGGAS FISGGTGTLY GINVGYDRFI 2160
 50 KGVIVGGYAA YGYSGFHANI TQSGSSNVNV GVSRAFIK SELTMSLNET WGYNKTFINS 2220
 YDPLLSIINQ SYRYDTWTTD AKINYGYDFM FKDKSVIFKP QVGLSYYYIG LSGLRGIMDD 2280
 PIYNQFRANA DPNKKSFLT NFALESRRHYF NKNSYFVIA DVGRDLFINS MGDKMVRFIG 2340
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55 <212> Type : PRT
 <211> Length : 2399
 SequenceName : SEQ ID 92
 SequenceDescription :

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 <213> OrganismName : Helicobacter pylori J99
 <400> PreSequenceString :

65 MEIQQTTHRK NRPLVSLVLA GALISAIPQE SHAAFFTTHVI IPAIVGGIAT GTAVGTVSGL 60
 LSWGLKQAE ANKTPDKPDK VWRIQAGKGF NEFPNKEYDL YKSLSSKID GGWDWGNAAR 120
 HYWVKGGQWN KLEVDMKDAV GTYKLSGLRN FTGGDLVNM QKATLRLGQF NGNSFTSYKD 180
 SADRTTRVNF NAKNISIDNF VEINNRVSGG AGRKASSTVL TLQASEGITS SKNAEISLYD 240

GATLNLASNS VKLNGNVWVG RLQYVGAYLA PSYSTINTSK VQGEVDFNHL TVGDQNAQA 300
GIIASNKTHI GTLDLWQSAG LNIIAPPEGG YKDKPNSTTS QSGTKNDKKE ISQNNNSNTE 360
VINPPNMTQK TETEPTQVID GPFAGGKDTV VNI FHLNTKA DGTIKVGGFK ASLTTNAAHL 420
NIGKGGVNLN NQASGRTLV ENLTGNITVD GPLRVNNQVG GYALAGSSAN FEFKAGVDTK 480
5 NGTATFNNDI SLGRFVNLKV DAHTANFKGI DTGNGGFNTL DFGSVTDKVN INKLITASTN 540
VAVKNFNINE LIVKTINGISV GEYTHFSEDI GSQSRINTVR LETGTRSIFS GGVKPKSCEK 600
LVINDFYYP WNYFDARNVK NVEITRFAS STPENPWGTS KLMFNNTLG QNAVMDYSQF 660
SNLTIQGDFI NNQGTINYLV RGGKVATLNV GNAAAMMFNN DIDSATGFYK PLIKINSAQD 720
LIKNTAEHVLK KAKIIGYGNV STGTNGISNV NLEEQFKERL ALYNNNNRMD TCVVRNTDDI 780
10 KACGMAIGNQ SMVNNPDNYK YLIGKAWRNI GISKANGSK ISVYVLGNST PTENGNTTN 840
LPTNTTNNAH SANYALVKNA PFAHSATPNL VAINQHDFGT IESVFELANR SKDIDTLYTH 900
SGAQGRDLLQ TLLIDSHDAG YARQMIDNTS TGEITKQLNA ATDALNNVAS LEHKQSGLOT 960
LSLSNAMILN SRLVNLRSKH TNHINSFAQR LQALKGQEFA SLESAAEVLY QFAPKYEKPT 1020
NVWANAIGGA SLNNGSNASL YGTSAGVDAF LNCNVEAIVG GFGSYGYSSF SNQANSLSNG 1080
15 ANNANFGVYS RPFANQHEFD FEAQAGLSD QSSLNFKSTL LQDLNQSYNY LAYSATARAS 1140
YGYDFAFFRN ALVLKPSVGV SYNHLGSTNF KSNSQSQVAL KNGASSQHLP NANANVEARY 1200
YYGDTSYFYL HAGVLQEFAL FGSNDVASLN TFKINAARSP LSTYARAMMG GELQLAKEVF 1260
LNLGVVYLHN LISNASHFAS NLGMRYSF 1288
<212> Type : PRT
20 <211> Length : 1288
SequenceName : SEQ ID 93
SequenceDescription :

Sequence
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NRYSTLNTLI KLSADPSAIN AVRENLGASA KNLIGDKANS PAYQAVLLAI NAAVGFWNVV 120
30 GYVTQCQGNA NGQKSISSTK IFNNEPGYRS TSITCSLNGH SPGYYGPMIS ENFKKLNEAY 180
QILQTALKRG LPALKENNGK VNVTYTYTCS GDGNMNCSSQ VTGVNNQKDG TKTKIQTIDG 240
KSVTTTSSK VVDSRADGNT TGVSYTEITN KLEGVPDSAQ ALLAQASTLI NTINNACPYF 300
HASNSSEANA PKFSTTTGKI CGAFSEEISA IQKMITDAQE LVNQTSVINE HEQTPVGN 360
NGKPFNPFTD ASFAQGMLAN ASAQAKMLNL AEQVGQAINP ERLSGTFQNF VKGFLATCNN 420
35 PSTAGTGGTQ GSAPGTVTQ TFASGCAYVG QTTNLKNSI AHFGTQEQQI QQAENIADTL 480
VNFKSYSEL GNTYNSITTA LSNI PNAQSL QNAVSKKNP YSPQIDTNY YLNQNSYNQI 540
QTINGELGRN PFRKVGIVSS QTNNGAMNGI GIQVGKQFF GQKRKGARY YGFFDYNHAF 600
IKSSFNSAS DVWYTGFGAD ALYNFINDKA TNFLGKNNKL SVGLFGGIAL AGTSWLNSEY 660
VNLATMNNVY NAKMNVANFQ FLFMGVRMN LARPKKKDS HAAQHGIELG LKIPTINTNY 720
40 YSFMGAELKY RRLYSVLYNY VFAY 744
<212> Type : PRT
<211> Length : 744
SequenceName : SEQ ID 94
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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MIKKAKKFI FFLIGSLLAE DNGWYMSVGY QIGGTQQFIN NKQLLENQNI INSITQSAIN 60
IAGPTTGLIT LSSQTVIDAL GYGVSNTVGN QLEGISNILN QIGKRKDFYS SRQISSISQ 120
IIGLKSSDP LKAHSSQITA KLLSNTQSAF DQGIALSSNI ISAVNSLNPS NNSQEVKAQL 180
QNTAQSMAL LQQIEHSITK TTSTTYAQL LSNTDAVNA SSNNTTYVSA LVNALNTLGV 240
GVFPTTSTH VVLNPPGQV FYPTNSLLGS TSSNSNNQQ YNNTLLMNTL QGELSTNNQN 300
55 NPNGCANQIQ CLEQFIQNL PLAATPTSTN QANQQVQAI QKLQSVAINA LDNNAINNTT 360
YNLNNLHNL NFQAYQSTIE QYNNALKQIS WISFSEPKNL LKNTSNNYQI GTVTNDQGN 420
ISAYDTSAT GSLSSDASSG ISCSATSTN NTNSFDNSLV ATSKVQTING KEQIGVNSFN 480
LVSQVSVYN SLKTSEENLQ KNAKILCNNG SQSGTSPCNS SSGGLSISGN AQLQNLSPT 540
NGTTTNTQAK SNASKLKAMV MVNNEEAKT TNFNQSSGPT TQSSNSTVMG ALNTVLQNVS 600
60 NFQQSIQSAF QNQENNIQAW ANALYNTSNP NGNQSQNLTT NNNQDLRIQL RANFYQLINT 660
INQQVPTDMN ALINQSQQT QTSQSASTN NACASGMSS GNCYQQWSD SKAYYSLQS 720
ALGYQTQATT QNGSSGGSNI TYNVQQITLT SGGLLNQIIT NLKSVNGGSN GGSSGNGTSQ 780
INTAYQMLTD ASDGKLGTYN SSNSNSSNS GNNNGYTPCN STNGSNGTSG SNCYEPNKQQ 840
NATTATTTT SNLQKVYNDA QKIANIASS GNNKGVENGL KQFFEALKSN SSSLSNLCGN 900
65 GSSGSSSTCS GGLINLLGAI PTNGVSDTNN LNLLETFIK TAGFIQNKDS NVSTSLTSAF 960
QAITSAISQ FQALQNDISP NAILTLLQEI TSNTTTIQSF SQTLLQLLGD KTFFMVQQL 1020
IDAMINARNQ VQNAQNQANN YGSQPVLSQY AAAKSTQHGM SNGLGVGIGY KYFFGKARKL 1080

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GLRHYFFFDY GFSEIGLANQ SVKANIFAYG VGTDFLWNLF RRTYNTKALN FGLFAGVQLG 1140
GATWLSLRLQ QIIDNWGNAN DIHSTNFQVA LNFGVRTNFA EFKRFAKKFH NQGVISQKSV 1200
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<212> Type : PRT
5 <211> Length : 1237
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    SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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VKNPQGIKAE ELAGLLNSTT TNNTNINIA GGNVAGTTLG NLFMNLQNL IDLYPTLKTN 120
15 NLHQCGSTNS GNGATAAAAT NNSPCFQGNL ALYNEMVDSI KTLNQNISKI IFQGDNNTTS 180
ANLSNQLSEL NTASVYLTYM NSFLNANNQA GGIFQNNNTQ AYENGVTAAQ IAYVLKQASI 240
TMGPSGDSGA AGAFLDAALA QHVFNANAG NDLSAKEFTS LVQNIIVNSQ NALTLANNAN 300
ISNSTGYQVS YGGNIDQARS TQLLNNTTNT LAKVTALNNE LKANPWLGNF AAGNSSQVNA 360
FNGFITKIGY KQFFGENKNV GLRYYGFFSY NGAGVGNNGPT YNQVNLLTYG VGTDLVLYNVF 420
20 SRSFGRSLN AGFFGGIQLA GDTYISTLRN SPQLASRPTA TKFQFLFDVG LRMNFGILKK 480
DLKSHNQHSI EIGVQIPTIY NTYYKAGGAE VKYFRPYSVY WVGYYAF 527
<212> Type : PRT
<211> Length : 527
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25 SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
30 <400> PreSequenceString :
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NTLNTLVKLS SDPSAVNDAR DNLGSSTRNL LDVKANSPAY QAVLLALNAA VGLWQVTSYA 120
FTACGPGSNE NANGGIQTFN NVPQGNTTTI TCNSYYEPGH GGPISTKNYA IINKAYQIIQ 180
KALTANGEGI PVLNNTTTKL DFTINGDKRT GGEPNKKLVY PWSHGKAIST SWNATITAPT 240
35 TENINTNSA QELLKQASII ITTLNSACPN FQNGGSGYWA GISGNGTMCQ MFKNEISAIQ 300
GMIANAQEAQ AQAKIVSENT QNQNSLDAGK PFNPYTDASF AESMLKNAQA QAEILNQAEQ 360
VVKNFKEIPT AFVNDSLGVC YEVQGGERRG TNPGQTTSNT WGAGCAYVGO TITNLKNSIA 420
HFGTQEQQIQ QAENIADTLV NFKSRYSELG NTYNSITTAL SNIPNAQSLQ NAVSKKNNPY 480
SPQGIDTNYI LNQNSYNQIQ TINQELGRNP FRKVGIVSSQ TNNGAMNGIG IQVGKQFFFG 540
40 QKRKGWARYY GFFDYNHAFI KSSFFNSASD VWTYGFADA LYNFINDKAT NFLGKNNKLS 600
VGLFGGIALA GTSWLNSEYV NLATMNNVYN AKMNVANFQF LFNMGVRMNL ARPKKKDSH 660
AAQHGIELGL KIPTINTNYI SFMGAELKYR RLYSVYLYNV FAY 703
<212> Type : PRT
<211> Length : 703
45 SequenceName : SEQ ID 97
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50 <213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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TNNILNNNTG GNVAGALSNA FSQYLYSLLG AYPYTKLNGD VSANALLSGA VSGTCAAAG 120
TAGGTTLNTQ SACTAAGYYW LPSLTDRILS TIGSQTYNGT NTNFPNMQQQ LTYLNAGNVF 180
55 FNAMNKALEK NGTATANSTS STSGATGSDG QTYSQQAIIQ LQGQQNINLN AANLLKQDEL 240
LLEAFNSAVA ANIGNKEFNS AAFTGLVQGI IDQSQLVYNE LTKNTISGSA VNNAGINSNQ 300
ANAVQGRASQ LPNALYNVQV TLDKINALNN QVRSMYPYLPQ FRAGNSRATN ILNGFYTKVG 360
YKQFFGKKRN IGLRYYGFFS YNGASVGFRS TQNNVGLYTY GVGTDVLYNI FRSYQNRSV 420
DMGFFSGIQL AGETFQSTLR DDPNVKLHGK INNTHFQFLF DFGMRMNFQK LDGKSNRHNQ 480
60 HTVEFGVVVP TIYNTYKSA GTTVKYFRPY SVYWSYGYSF 520
<212> Type : PRT
<211> Length : 520
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<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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TNYSVLNALI RQADPNAIN NARGNLNASA KNLINDKNS PAYQAVLLAL NAAAGLWQVM 120
5 SYAISPCCPG KDTSKNGGVQ TFHNTPSNQW GGTITTCGTT GYEPGPYSIL STENYAKINK 180
AYQIIQKAFG SSGKDIPALS DTNTELKFTI NKNNGTNTN NNGEEIVTKN NAQVLEQAS 240
TIITTLNSAC PWINNGGAGG ASSGSLWEGI YLKGDSACG IFKNEISAIQ DMIKNAIAV 300
EQSKIYAANA QNQRNLDTGK TFNPYKDANF AQSMFANAKA QAEILNRAQA VVKDFERIPA 360
EFVKDSLGVG HEVQNGHLRG TPSGTVTDNT WGAGCAYVGE TVTNLKDSIA HFGDQAERIH 420
10 NARNLAYTLA NFSSQYQKLG EHYDSITAAI SSLPDAQSLQ NVVSKKTNPV SPQGIQDNY 480
IDSNISQVQ SRQELGSPN FRRAGLIAAS TTNNGAMNGI GFQVGYKQFF GKNKRWGARY 540
YGFVDYNHTY NKSQFFNASS DVWTVGVGSD LLVNFINDKA TKHNKISFGA FGGIALAGTS 600
WLSQVYVLA NVNNYYKAKI NTANFQFLFN LGLRMLNARK KHRATDNAAQ HGIELGKIP 660
TINTNYSSL-GTTLQYRRLY SVYLVYVFAY 690
15 <212> Type : PRT
<211> Length : 690
SequenceName : SEQ ID 99
SequenceDescription :
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<213> OrganismName : Helicobacter pylori J99
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25 LNQYNYLNSL VNLASTPSAI TGAIDNLSST AINLTSATTT SPAYQAVALA LNAAVGMWQV 120
IAFGISCGPG PNLGPEHLEN GGVRSDNTN NYSYNTGSGT TTTTCNGASN VGPNGILSSS 180
EYQVLNTAYQ TIQTALNQNG GGGMPALNSS KNMVNVINQT FTKNPTTEYT YPDGNGNYYS 240
GGSSIPIQLK ISSVNDANL LQQAATIIINV LTTQNPVNG GGGAWGFGGK TGNVMDIFGD 300
SFNAINEMIK NAQAVLEKTQ QLNANENTQI TQPDNPNPYT SKDTQFAQEM LNRANAQAEI 360
30 LSLAQVADN FHSIQGPIQQ DLEECTAGSA GVINDNTYGS GCAFVKETLN SLEQHTAYYG 420
NQVNQDRALS QTLNFKAL STLGNDSKAI NSGISNLPNA KSLQNMTHAT QNPNSPEGLL 480
TYSLDTSKYN QLQTVQELG KNPFRIRIGVI NYQNNNGAMN GIGVQAGYKQ FFGKKRNWGL 540
RYYGFFDYNH AYIKSNFFNS ASDVWTVGVG MDALYNFIND KNTNFLGKNN KLSVGLFGGF 600
ALAGTSWLNS QQVNLTMNG IYNANVSASN FQFLFDLGLR MNLARPKKKD SDHAAQHGM 660
35 LGVKIPTINT DYYSFMGAEL KYRRLYSVYL NYVFAY 696
<212> Type : PRT
<211> Length : 696
SequenceName : SEQ ID 100
SequenceDescription :
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<213> OrganismName : Helicobacter pylori J99
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45 MKIKKSLFAL SFSLMASLSR AEDDGFYMSV GYQIGEAQVK VKNTGALQNL ADRYDNLSNL 60
LNQYNYLNSL VNLASTPSAI TGAIDNLSST AINLTSATTT SPAYQAVALA LNAAVGMWQV 120
IAFGISCGPG PNLGPEHLEN GGVRSDNTN NYSYNTGSGT TTTTCNGASN VGPNGILSSS 180
EYQVLNTAYQ TIQTALNQNG GGGMPALNSS KNMVNVINQT FTKNPTTEYT YPDGNGNYYS 240
GGSSIPIQLK ISSVNDANL LQQAATIIINV LTTQNPVNG GGGAWGFGGK TGNVMDIFGD 300
50 SFNAINEMIK NAQAVLEKTQ QLNANENTQI TQPDNPNPYT SKDTQFAQEM LNRANAQAEI 360
LSLAQVADN FHSIQGPIQQ DLEECTAGSA GVINDNTYGS GCAFVKETLN SLEQHTAYYG 420
NQVNQDRALS QTLNFKAL STLGNDSKAI NSGISNLPNA KSLQNMTHAT QNPNSPEGLL 480
TYSLDTSKYN QLQTVQELG KNPFRIRIGVI NYQNNNGAMN GIGVQAGYKQ FFGKKRNWGL 540
RYYGFFDYNH AYIKSNFFNS ASDVWTVGVG MDALYNFIND KNTNFLGKNN KLSVGLFGGF 600
55 ALAGTSWLNS QQVNLTMNG IYNANVSASN FQFLFDLGLR MNLARPKKKD SDHAAQHGM 660
LGVKIPTINT DYYSFMGAEL KYRRLYSVYL NYVFAY 696
<212> Type : PRT
<211> Length : 696
SequenceName : SEQ ID 101
SequenceDescription :
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<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
65 MHKKVLALT ASLICQESLF AKDKDYTLGK VSTAGKKDRS DYSGQVNLGY SGITAPKSWQ 60
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SGHSDATLML VNGIPVYMAP YAHIELDIFP VTFQAIIDRID VIKGGGSVQY GPNTYGGIVN 180
IITKPIPNQW ENQAAERITY WAKARNAGFA APPDKTGDP S FIKSLGNNLL YNTYVRSGGM 240
INKHVGIIAQ ANWVRGQGFR DNSPSSISNY WLDGVYDINE SNGIKAYYQY YDFAIAPQGS 300
LSEQDYKINR FANLRPLNOK GGRSQRFGAV YENRFGDLDR VGGTFSFTYY GQLMTRDFQV 360
5 SSSYNSANMV TCFSEAACRA AGLPAGYNLA VPYYATNYNG WAEVENPVRS INNAFEPKVN 420
LIVNTGKVRQ TFIMGLRFMT TTFLQRQYLN TNECATKTS G EGAGFLCEGP NVMSGWKPHI 480
KHGVYRNWNN WRNNYTAVYL SDRIEAWDGR FFIVPGLRYA FVQYNNENAS NWMQIPEKDL 540
RKIKHMNNWM PSTNIGFIPV QGDHNVLT YF NYQSFVFPQ LDVLSYGGAE YFTQHFDTVE 600
AGARYTYKDK FSVNADYFRI WARDFATGQY SVYTS GPMKG NVRPINGYSQ GVELELYYRP 660
10 IRGLQFHAAF NYIDTRVTSH GPLTDLNGDV LKGTSYNKH F PFVSPFQFIF DARYNWRKTT 720
IGISSYFYSR AYSGISNSAA GGYYGMYYS GGNNYESVLN SGYQCEAWCM TQHEGLLPWY 780
WVWNIQVSQI FWENGRHRVT GSLQINNIFN MKYYFTGIGS SPAGLQPAPG RSVTAYLNYT 840
F 841
<212> Type : PRT
15 <211> Length : 841
SequenceName : SEQ ID 102
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<400> PreSequenceString :
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25 VQCGPGNSGQ QSVTFEGQPG HNSSSINCNL TGYNNGVSGP LSIENFKKLN QAYQTIQQAL 180
KQDSGFPVLD SAGKQVTITI TTQTNGANKS ETTTTTTTTN DAQTLLEAS KMISVLTNC 240
PWVNHNNQGN GGAPWGLDTA GNVQCVFATE FSAVTSMIKN AQEIVTQAQS LNQQNNQNAP 300
QDFNPYTSAD RAFAQNMLNH AQAQAKILEL ADQMKDLNT IPSQFITNYL AACHNGGGTL 360
PDAGVTNNTW GAGCAYVEET ITALNNSLAH FGTQAEQIKQ SELLARTILD FRGSLSNLNN 420
30 TYNSITTTAS NTPNSPFLKN LISQSTNPNM PGGLQAVYQV NQSAYSQLLS ATQELGHNPF 480
RRVGLISSQT NNGAMNGIGV QVGKQFFGE KRRWGLRYYG PFDYNHAYIK SSFFNSASDV 540
FTYGVGTDVL YNFINDKTTK NSKISFGVFG GIALAGTSWL NSQYVNLATF NNFYSAKMNV 600
ANFQFLFNLG LRMNLAKNKK KASDHAAQH G VELGVKIPTI NTNYYSLLTG QLQYRRLYSV 660
YLNYYVFAY 668
35 <212> Type : PRT
<211> Length : 668
SequenceName : SEQ ID 103
SequenceDescription :

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45 ILKRAANLFT NAEATSKLKF SSLSPVRVLY MYNGQLTIEN FLPPYLNNNVK LSFTDAQGNT 120
IDLGVIETIP KHSKIVLPGE AFDLKEAFD KIDPYTLFLP KFEATSTSTIS DTNTQRFVET 180
LNNIKTNLIM KYSNENPNNF NTCPPYNNNGN TKNDWCQNFT PQTAEEFTNL MLNMI AVLDS 240
QSWGDAIINA PFEFTNSSTD CSDSPSKCVN PGVNGRVDTK VDQYILNKQ GIINNFRKKI 300
EIDAVVLKNS GVVGLANGYG NDGEYGTGLV EAYALDPKKL FGNDLKTINL EDLRTILHEF 360
50 SHTKGYGHNG NMTYQRPVPT KDGQVEKDSN GKPKDSGLP YNVCSLYGGS NQPAFPSNYP 420
NSIYHNCADV PAGFLGVTA VVQQLINQNA LPINYANLGS QTYNINLNASL NTQDLANSML 480
STIQKTFVTS SVTNHHFSNA SQSFRSPILG VNAKIGYQNY FNDFIGLAYY GIIKYNKYA 540
VNQKVQQLSY GGGIDLLDF ITTYSNKNSP TGIQTKRNF SSGGIFGGLR GLYNSYYVLN 600
KVKGSGNLDV ATGLNRYKH SKYSVGISIP LIQRKASVVS SGGDYTNSFV FNEGASHFKV 660
55 FFNYGWVF 668
<212> Type : PRT
<211> Length : 668
SequenceName : SEQ ID 104
SequenceDescription :

Sequence
60 -----
<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
65 MNKTTIKILM GMAILSSLQA AEAELDEKSK KPKFADRNTF YLGVGYQLSA INTSFSTSSI 60
DKSYFMTGNG FGVVLGGKFV AKTQAVEHV G FRYGLFYDQT FSSHKSIST YGLEFSGLWD 120
AFNSPKMFLG LEFGLGIAGA TYMPGGAMHG IIAQYLKEN SLFQLLVKVG FRFGFFHNEI 180

TFGLKFPVIP NKKTEIVDGL SATTLWQRLP VAYFNYIYNF 220
<212> Type : PRT
<211> Length : 220
SequenceName : SEQ ID 105
5 SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
10 <400> PreSequenceString :
MKKTCKKTILL SLTLAASLLH AEDNGVFLSV GYQIGEAVQK VKNADKVQKL SDVYEQLSKL 60
LANDNGTSSK TSAQAINQAV NNLNESAKTL AGGTTNSPAY QATLLALRSA LGLWNSMGYA 120
VVCGGYIKKP GENNQKNFHY TDENGNGTTI NCGGSTNSNG THSPNGTNTL KADKNVSLSI 180
EQYEKIHEAY QILSKALKQA GLAPLNSKGE KLEAHVTTSK DQOGTSSDQT TTTTSVIDTT 240
15 NDAQNLLTQA QTIVNTLKDY CPMLIAKSSS NGGTNGANTP SWQTAGGGKN SCATFGAEFS 300
AISDMISNAQ KIVQETQQLN ANQPKNITQP NNFNLNSPGS LTALAQSMLEK NAQSQTLEIK 360
LANQVADDFD LSSSGYLKDY IGKCDVSGVS SSNMTPQNMN TTWGGKGCAGV EETLTSLEKAS 420
TTDFNNQTTT QLDQAQTLAN TLTQELGNPP FKRVGIIIGSQ TNGGAMNGLG VQAGYKQFFG 480
QKRRLWGLRYY GFFDYNHTYI KSSFFNSSSD VLTGTVGSDL LFNFNINDKNT NFLGKNNKIS 540
20 VGLFPGGIALA GTSWLSNQFV NLKTTISNVYS AKVNTANFQF LFNGLRLTNL ARPKKKDSDH 600
SAQHGMELGV KIPTINTNYY SYLGTKLEYR RLYSVYLYNVF FAY 643
<212> Type : PRT
<211> Length : 643
SequenceName : SEQ ID 106
25 SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
30 <400> PreSequenceString :
MKKTILLSLM VSSLFAENDG VYMSVGQIG EAAQMVKN TG EIQKVSNA YE NLNNLLTRYN 60
ELKQTASNTD SSTAQAIDNL EKSASRLKTT PMTANQAVSS ALSSAVGMWQ VIASNLANS 120
LSSSEYEKLEK ATSQLLQNTL ENKNNNLKIE NDYDQLLTQA STIINTLQSQ CPGVDGGNGK 180
PWGINTSGNA CAIFGSTFNA INSMIDSAKK AAADARRTAP ESPNQNAFT NADFNKNLNQ 240
35 VSSVINDTIS YLKGDNLETI YNTIQKTPNS KGFSQSLVRS SYSYSLNETQ YSQFQTTTKE 300
FGHNPPFRSVG LINSQSNGA MNGVGVQLGY KQFFGKKNKFF GIRIYGFDDY NYAYIKSNFF 360
NSASNVFTYG AGSDLLNFI NGGSDRNRKV SFGIFGGIAL AGTTWLNNQS ANLKITNSAY 420
SAKINNTNFQ FLFNTGLRLQ GIHHGIELGV KIPTINTNYY SFMGAKLAYR RLYSLYLYNVF 480
LAY 483
40 <212> Type : PRT
<211> Length : 483
SequenceName : SEQ ID 107
SequenceDescription :

45 Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MPKASQVLFF GAFLSTSLQG FEAKLNGFVD QSSTIGFNQH KINKERGIYP MQQFATIAGY 60
50 LGLGFSLLPK KVDHVLKKG IGGMVGSIFY DGTCKKFEDGS VAYNLFGYYD GFMGVYTNIL 120
QTDSLETQNM KHNKNVRNYV FSDAYLEYAY KNYFEIKAGR YLSTMPYKSG QTQGFQVSGQ 180
YKHARLTWFS SWGRAFYGS FLMDWFAART TYSGGFTKNN NGGYDSHGRK VLYGTHAVQL 240
TYKPHRFLIE GFYYLSPQIF NAPGVKIGWD SNPNFSGTGF RSDTAIGFF PIYYPWMIVK 300
SNGSPVYRYD TPATQNGQNL IIRQRFDINN YNVSIIFYKV FQANGWIGN MGNPSGVIMG 360
55 SNSVYAGFTG TALKRDAATI FLSCGGTHFA KKFTWKFTQ YSNSVVSWEA RAMISLGYKF 420
TEYLSGSVDL AYYGVHTNKG FKPGENGPPV KNFPALYSR SALYTALVAS F 471
<212> Type : PRT
<211> Length : 471
60 SequenceName : SEQ ID 108
SequenceDescription :

Sequence

65 <213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MLRLVSKTIC LSLISLFNPL EAFQKHQKDV FFVEAGFETG LLEGAQTKEQ AIAQNTQNTQ 60

KIYENPLTHP QTKEQPKEQN KSDTATPQSV YGRYYILQNT ILEKATELFT AANINGNGLT 120
FYSQNPVYVM AYNKDNAEFE GYGNNNSVVVI QNFLPYNLNN IELSYTDAQG KAVNLGVIET 180
IPKDSQIILP ASLFNNFSND SPFNSDGLQQ LQTTTTPFSD ANTQSLFEKL SQITTNLQMT 240
YENTDPFSSG NNDPNGPLAS PKPHYECPGY KKSCQVASVS FTPQTAEELT NLMLDMIAVF 300
5 DSKSWEEAVL NAPFQFSNSP SECGIDYPKC VNPFFNGLVD PKDEKYALTPEEVINSYRVA 360
NELTVNLLNA AKGFLGLGSQ LGSANAPDDD GFNQGVLGIA PFALDPEKLF GKNLNKVAIL 420
ALRDIIEHYG HTLGYTHNGN MTYQVRVLCQ EGNNGPEARCE GCHEVEKNGK EELEFSNGHE 480
VRDHDGYTYD VCSRFGGKNQ PAFPSNY PNS IYTNCAQVPA GLIGVTTAVW QQLINQNALP 540
INFANLNSQT SHLNAGLNAQ NFATSMVSAI AQNFSTSTT TYRSSSKNFR SPILGVNVKI 600
10 GYQHYFNDYI GLAYYGIQY NYAQANDEKI QQLSYGGMD VLFDFITTYT NKKQDHPTKK 660
VFASSFGVFG GLRGLYNSY VFNQVKSGN LDIVTGFNYR YKHSKYSIGV SVPLIQSGIK 720
IASNNGIYAD SVVLNEGSH FKVFFNYGWV F 751
<212> Type : PRT
<211> Length : 751
15 SequenceName : SEQ ID 109
SequenceDescription :

Sequence

20 <213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MQNFVFNKKW LIYSSLLPLF FLNPLMAEDD GFFMGVSYQT SLAVQRVDNS GLNASQDAST 60
YIRQNAIALE SAAVPLAYYL EAMGQQTRVL MQMLCPDFSK RCLLYAGGVQ NGQNNNGDTG 120
NNPPRGVNVA TFDMSQLVNN LNKLTQLIGE TLIRNPENLP NSKVFNKFG NQSTVIALPE 180
25 GLANTMDALN NDIITNLTTL WYNQTLTNKS FSTPSNTSVN FSPQVLQHLL QDGLATANNN 240
QTICSTQMQC TATNEAKSIA QNAQNIFQAL MQAGILGGLA NEKQFGFTYN KAPNGSDSQ 300
GYQSFSGPGY YTKNDNTTQA PLKALPAGAT IGSGNGQYTY HPSSAVVYLA DSIIANGITA 360
SMIFSGMQNF ANKAAKLIGT SSYNQMQDAI NYGESLLENT VAYGDFITNW VAPYLDLNNK 420
GLNFLPNYGG QLNAGANNQTP QLTPQQAQQE QKVINMQLEQ ATNAPTPAQI NRILANPYSP 480
30 TAKTLMAYGL YRSKAVIGV IDEMQTKVNO VYQMGFARNF LEHNSNSNNM NGFGVKMGYK 540
QFFGKKRMFG LRYGYFYDFG YAQFGTESSL VKATLSSYGA GTDFLYNVFT RKRGTETADI 600
GFFAGIQLAG QTWKTNFLDQ VDG NHLKPKD TSFQFLFDLG IRTNFSKIAH QKRSRFSQGI 660
EFGLKIPVLY HTYYQSEGV T AKYRRDFSFY VGYNIGF 697
<212> Type : PRT
35 <211> Length : 697
SequenceName : SEQ ID 110
SequenceDescription :

Sequence

40 <213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKKTILLSLS LSLASSLLHA EDNGFFVSAG YQIGEAVQMV KNTGELKNLN EKYEQLSQYL 60
NQVASLKQSI QNANNIELVN SSLNYLKSFT NNNYNSTQS PIFNAVQAVI TSVLGFWSLY 120
45 AGNYLTFFV NKDTQKPASV QGNPPFSTIV QNCSGIENCA MNQTTYDKMK KLAEDLQAAQ 180
QNATTKANNL CALSGCATTQ GQNPSSSTVSN ALNLAQQLMD LIANTKTAMM WKNIVIAGVS 240
NVSGAIDSTG YPTQYAVFNN IKAMIPILQQ AVTLSQSNHT LSASLQAQAT GSQTNPKFAK 300
DIYAFANQK QVISYAQDIF NLFSSIPKQD YRYLEKAYLK IPNAGKTPTN PYRQEVNLNQ 360
EIQTIQNNVS YYGNRVDAAL SVAKDVPNK SNQTEIVTTY NNAKNLSQEI SKLPYNQVNT 420
50 KDIITLPYDQ NAPAAGQYNY QINPEQQSNL SQALAAMSNN PFKKVGMISS QNNNGALNGL 480
GVQVGYKQFF GESKRWGLRY YGFFDYNHGY IKSSFFNSSS DIWTYGGGSD LLVNFINDSI 540
TRKNNKLSVG LFGGIQLAGT TWLNSQYMN L TAFNNPYSAK VNASNQFLF NLGLRTNLAT 600
AKKKDSERSA QHGVELGIKI PTINTNYYSF LGTKLEYRRL YSVYLNIVFA Y 651

55 <212> Type : PRT
<211> Length : 651
SequenceName : SEQ ID 111
SequenceDescription :

60 Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MLKLASKTIC LSLISSFTAV EAFQKHQKDG FFIEAGFETG LLQGTQTQEQ TIATTQEKPK 60
65 PKPKPKPITP QSTYGYKYYIS QSTILKNATE LFAEDNITNL TFYSQNPVYV TAYNQESAEE 120
AGYGNNSLIM IQNFLPYNLN NIELSYTDDQ GNVVSLGVIE TIPKQSQIIL PASLFNDPQL 180
NADGFQQLQT NTTRFSDAST QNLFNKLSKV TTNLQMTYIN YNQFSSGNGS GSKPPCPPYE 240

5 NQANCVAKVP PFTSQDAKNL TNMLMLNMAV FDSKSWEDAV LNAPFQFSDN NLSAPCYSDY 300
LTCVNPYNDG LVDPKLIAKN KGDEYNIENG QTGSVILTPQ DVIYSYRVAN NIYVNLPLPTR 360
GGDLGLGSQY GGPNGPGDDG TNFGALGILS PFLDPEILFG KELNKVAIMQ LRDIIHEYGH 420
TLGYTHNGNM TYQVRMCEE NNGPEERCQG GRIEQVDGKE VQVFDNGHEV RDTDGSTYDV 480
5 CSRFKDKPYT AGSYPNISYT DCSQVPAGLI GVTSVAVWQQL IDQNALPVDF TNLSSQTNVL 540
NASLNTQDFA TTMLSAISQS LSSSKSSATT YRTSKTSRPF GAPLLGVNLK MGYQKYFNDY 600
LGLSSYGIK YNYAQANNEK IQQLSYGVGM DVLFDFITNY TNEKNPKSNL TKKVFTSSLG 660
VFGGLRGLYN SYLLNQYKG SGNLNVGTGL NYRYKHSKYS IGISVPLVQL KSRIVSSDGA 720
YTNSITLNEG GSHFKVFFNY GWIF 744

10 <212> Type : PRT
<211> Length : 744
SequenceName : SEQ ID 112
SequenceDescription :

15 Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
20 MRKLFIPLLL FSALEANENK GFFIEAGFET GLLEGTQTQE KRHTTTKNTY ATYNYLPTDT 60
ILKRAANLFT NAEAISKLKF SLSLSPVRVLY MYNGQLTIEN FLPYNLNNVK LSFTDAQGNV 120
IDLGVITIP KHSKIVLPGE AFDSLKIDPY TLFLPKIEAT STSISDANTQ RVFETLNKIK 180
TNLVVNYRNE NKFKDHENHW EAFTPQTAE F'TNLMLNMIA VLDSQSWGDA ILNAPFEFTN 240
SPTDCDNDPS KCVNPGTNGL VNSKVDQKYV LNKQDIVNKE KNKADLDVIV LKDSGVVGLG 300
SDITPSNNDG GKHYGQLGVV ASALDPKKLF GDNLKTINLE DLRTILHEFS HTKGYGHNGN 360
25 MTYQRVPVTK DGQVEKDSNG KPKDSGLPY NVCSLYGGSN QPAFPSNYPN SIYHNCADVP 420
AGFLGVTA AV WQQLINQNAL PINYANLGSQ TNYNLNASLN TQDLANSMLS TIQKTFVTSS 480
VTNHHFSNAS QSFRSPILGV NAKIGYQNYF NDFIGLAYYG IIKYNYAKAV NQKVQQLSYG 540
GGIDLLLDLI TTYSNKNSTP GIQTKRNFSS SFGIFGGLRG LYNYSYVLNK VKGSGNLDVA 600
TGLNRYKHS KYSVGISIP LQRKASVVSS GGDYTNSTFV NEGASHFKVF FNYGWVF 657

30 <212> Type : PRT
<211> Length : 657
SequenceName : SEQ ID 113
SequenceDescription :

35 Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
40 MSLATSYNVS NNFSKFNIKR VRGYLICLVC NTPKMIQRGL NGVSFYGCSD YVNGKDCKGV 60
LREINGSMKM VCLHCENTPI MEKVESGRGG AYACKNCNRK FYFIDLAKQN ERKKOLEKEK 120
KELLNKIEKQ KIKHLERFIL AGVKANIKEN SFPLGCKNYP KCEWTASMDS QDLKCPKCNR 180
LMKRKKNFKN NEFFTATSLT LNAIEFCLYI NLKKKETNV 219

45 <212> Type : PRT
<211> Length : 219
SequenceName : SEQ ID 114
SequenceDescription :

50 Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
55 MEIKKYFLYA LFFLLFSGLF LSKLQAYKFN MSIVGKVSSY TKFGFNNQRY QPSKDIYPTG 60
SYTSLLGELN LSMGLYKGLR AEVGAMMAAL PYDSTAYQGN NIPNGQPGSR TDPFGAGIFW 120
QYIGWYAGHS GLNVQKPRLA MVHNAFLSYN YKKDKFSFGV KGGRYDAEEY DWFTSYTQGV 180
EGFVKYKDTR LRVMYSDARA SASSDWFYF GRYYTSGKAL MIADLKYEK NLKINPYFYA 240
IFQRMYPAGI NITYDTNP NF NNKGFRFVGT FVGFFPIFAT PANQNDIILF QQVPLGKSGQ 300
TYFFRTRFYY NKWQFGGSVY KNIGNANGDI GIYGDPLGYN IWTNSIYDAE INNIVGADVI 360
NGFLYVGSQY RGFWSKILGR WTDSPRADER SLALFLSYFS NKYNIRMDLK LEYYGNITKK 420
60 GYCIGYCGMY VPDVDPNGPGT QPLTHNVYS RSHIMFNITY GFRIY 465

<212> Type : PRT
<211> Length : 465
SequenceName : SEQ ID 115
SequenceDescription :

65 Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKKTILLSLS LSLASSLLHA EDNGFFVSAG YQIGEAQVMV KNTGELKNLN DKYEQLSQSL 60
AQLASLKSKI QTANNIQAVN NALSDLKSFA SNNHTNKETS PIYNTAQAVI TSVLAFWSLY 120
5 AGNALS FHVH GLNDGNSNPL GRIHRDGNCT GLQQCFMSKE TYDKMKTLAE NLQKAQGNLC 180
ALSECSSNQS NGGKTSMTTA LQTAQQLMDL IEQTKVSMVW KNIVIAGVTN KPNGAGAIT 240
TGHVTDYAVF NNIKAMPLIL QQALTLSQSN HTLSTQLQAR AMGSQTNREF AKDIYALQN 300
QKQILSNASS IFNLFNISIPK DQLKYLENAY LKVPHLGKTP TNPYRQNVNL NKEINAVQDN 360
VANYGNRLDS ALSVAKDVYN LKSNQTEIVT TYNDAKNLSE BISKLPYNQV NVTNIVMSPK 420
10 DSTAGQYQIN PEQQSNLNQA LAAMSNNPFK KVGMISSQNN NGALNGLGVQ VGYKQFFGES 480
KRWGLRYYGF FDYHNGYIKS SFFNSSSDIW TYGGGSDLLV NFINDSITRK NNKLSVGLFG 540
GIQLAGTTWL NSQYMNLTAF NNPYSAKVNA SNFQFLFNLG LRTNLATAKK KDSERSAQHG 600
VELGIKIPTI NTNYSFSLGT KLEYRRLYSV YLNYVFAY 638
<212> Type : PRT
15 <211> Length : 638
SequenceName : SEQ ID 116
SequenceDescription :

Sequence

20 <213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKLKKRKVAA TLLKRLTLPL LFTTGS LGAV TYEVHGDFIN FSKVGFNRSP INPVKGIYPT 60
ETFVNLTGKL EGSVHLGRGW TVNVGGVLGG QVYDNTRYDR WAKDFTPPSY WDKTSCGTDS 120
25 LSLCMNATKM WQQQGGPGII DPERGIGYMYM GEWNGLFPNY YPANAYLPGH SRRYEVYKAN 180
LTYDSDRVHM VMGRFDVTEQ EQMDWIYQLF QGFYGTFFKLT KNMKFLLFSS WGRGIADGQW 240
LFPIYREKPW GIHKAGIYR PTKNLMIHYP VYLIPMVGTL PGAKIEYDTN PEFSGRGIRN 300
KTTFFVLYDY RWNNAEYGRY APARYNTWDP FLDNGKWRGL QGPGGATLYL HHHIDINNYF 360
VVGAYLNLG NPNMNLGTWG NPVALDGIEQ WVGGIYSLGF AGIDNITDAD AFTEYVKGEG 420
30 KHGKFSWSVY QRFTTAPRAL EYGIGMYLDY QFSKHVKAGL KLVWLEFQIR AGYNPGTGFL 480
GPNQQLPLN NGLFESSAFA QGPQNMGGIA KSITQDRSHL MTHISYSF 528
<212> Type : PRT
<211> Length : 528
SequenceName : SEQ ID 117
SequenceDescription :

Sequence

35 <213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKNFSPLYCL KKLKKRHLIA LSLPLLSYAN GFKIQEQSLN GTALGSAYVA GARGADASFY 60
NPANMGFTND WGENRSEFEM TTTVINIPAF SFKVPTTNQG LYSVTSLEID KSQONILGII 120
NTIGLGNILK ALGNTAATNG LSQA INRVQG LMNLTNQKV TLASKPDTQI VNGWTGTNPF 180
45 VLPKFFYKTR THNGFTFGGS FTAPSGLGKMK WNGKGGEFLH DVFIMMVELA PSMSYTINKR 240
FSVGVLRLGL YATGSFNNTV YVPLEGASVL SAEQILNLPN NVFADQVPSN MMTLLGNIGY 300
QPALNCQKAG GDMSDQSCQE FYNGLKKIMG YSGLIKASAN LYGTTQVVQK SNGQGVSGGY 360
RVGSSLRVFD HGMFSVVYNS SVTFNMKGGL VAITELGPSL GSVLTKGSLN INVSLPQTLS 420
LAYAHQFFKD RLRVEGVFER TFWSQGNKFL VTPDFANATY KGLSGTVASL DSETLKKMVG 480
LANFKSVMNM GAGWRDTNTF RLGVTYMGKS LRLMGIDYD QAPSPQDAIG IPDSNGYTVA 540
50 FGTKYNFRGF DLGVAGSFTF KSNRSSLYQS PTIGQLRIFS ASLGYRW 587
<212> Type : PRT
<211> Length : 587
SequenceName : SEQ ID 118
SequenceDescription :

Sequence

55 <213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
60 MAFQVNTNIN AMNAHVQSAL TQNALKTSLE RLSSGLRINK AADDASGMTV ADSLRSQASS 60
LQQA IANTND GMGIIQVADK AMDEQLKILD TVKVKAQAA QDGQTESRK AIQSDIVRLI 120
QGLDNIGNTT TYNGQALLSG QFTNKEFQVG AYSNQSIKAS IGSTTSKIG QVRIATGALI 180
TASGDISLTF KQVDGVNDVT LESVKVSSSA GTGIGVLAEV INKNSNRTGV KAYASVITTS 240
DVAVQSGSLS NLTLNGIHLG NIADIKKND DGRLLVAANA VTSETGVEAY TDQKGRNLNR 300
65 SIDGRGIEIK TDSVSNGPSA LTMVNGGQDL TKGSTNYGRL SLTRLDAKSI NVVSASDSQH 360
LGFTAIGFGE SQVAETTVNL RDVTGNFNAN VKSASGANYN AVIASGNQSL GSGVTTLRGA 420
MVVIDIAESA MKMLDKVRSD LGSVQNQMIS TVNNISITQV NVKAAESQIR DVDFAEESAN 480

FNKNNILAQS GSYAMSQANT VQONILRLLT 510
<212> Type : PRT
<211> Length : 510
SequenceName : SEQ ID 119
5 SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
10 <400> PreSequenceString :
MAGTQAIYES SSAGFLSQVS SIISSTSGVA GPFAGIVAGA MTAALPIVV GFTNPQMTAI 60
MTQYNQSIAS AVSVPKMAAN QQYNQLYQGF NDQSMVAVGNN ILNISKLTGE FNAQGNTQSA 120
QISAVNSQIA SILASNTTPK NPSAIEAYAT NQIAVPSVPT TVEMMSGILG NITSAAPKYA 180
LALQEQLRSQ ASNSSMNDTA DSLDSC TALG ALVGSSKVFF SCMQISMTPM SVSMPTVYAK 240
15 YQAVATKALT SGVNPMTTPA CPIGDKVLAV YCYAEKVAEI LREYYIEFVK NNTNLLQNAS 300
QMILNQSGLA TSTYDTQAIS NISSLYNYNI VANKSFLKSH LTYLDYIKDK LKGQKDSYLT 360
ERVQTKLIVK 370
<212> Type : PRT
<211> Length : 370
20 SequenceName : SEQ ID 120
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
25 <400> PreSequenceString :
MTNEAINQQP QTEAAFNPQQ FINNLQVAFI KVDNVVASFD PNQKPIVDKN DRDNRQAFEK 60
ISQLREEFAN KAIKNPTKKN QYFSSFISKS NDLIDKDNLI DTGSSIKSFQ KFGTQRYQIF 120
MNWVSHQNDP SKINTQKIRG FMENIIQPPI SDDKEKAEFL RSAKQAFAGI IIGNQIRSDQ 180
30 KFMGVFDESL KERQEAENKNG EPNGDPTGGD WLDIFLSFVF NKKQSSDLKE TLNQEPVPHV 240
QPDVATTTTD IQSLPPEARL LDERGNFSK FTLGDMNMLD VEGVADIDPN YKFNQLLIHN 300
NALSSVLMSG HNGIEPEKVS LLYGNNGGPE ARHDWNATVG YKNQRGDNVA TLINVHMKNK 360
SGLVIAGGEK GINNPSFYLY KEDQLTGSQR ALSQEEIQNK VDFMEFLAQN NAKLDNLSKK 420
EKEKFQNEIE DFQKDSKAYL DALGNDHIAF VSKDKKKHLA LVAEFGNGEL SYTLKDYGKK 480
35 ADKALDREAK TTLQGS LKHD GVMFVDYSNF KYTNASKSPD KGVGATNGVS HLEAGFSKVA 540
VFNLPLNLNL AITSVVRQDL EDKLIAGKLS PQEANKLVKD FLSSNKELVG KALNFNKAVA 600
BAKNTGNYDE VKQAQKDLEK SLKKRERLEK DVAKNLESKS GNKNKMEAKS QANSQKDEIF 660
ALINKEANRD ARAIAYAQNL KGIKRELSDK LENINKDLKD FSKSFDEFKN GKNKDFSKAE 720
ETLKALKGSV KDLGINPEWI SKVENLNAAL NEFKNGKNKD FSKVTQAKSD LENS IKDVII 780
40 NQKITDKVDN LNAQSVS VAKA TGDFSGVEQA LADLKNFSKE QLAQQAQKNE DFNTGKNSAL 840
YQSVKNGVNG TLVGNGLSKA EATTL SKNFS DIKKELNAKL GNFNNNNNNG LENSTEPIYT 900
QVAKKVKAKI DRLDQIASGL GDVGQAASFL LKRHDKVDDL SKVGLSANHE PIYATIDDLG 960
GPFPLKRHDK VDDL SKVGLS REQKLTQKID NLNQAVSEAK ASHFDNLDQM IDKLKDS TKK 1020
NVVNLVYVESA KKVPTSLSAK LDNYATNSHT RINSNVKNGT INEKATGMLT QKNSEWLKLV 1080
45 NDKIVAHNVG SAPLSAYDKI GFNQKNMKDY SDSFKFSTRL SNAVKDIKSG FVQFLTNI FS 1140
MGSYS LMKAS VEHGVKNTNT KGGFQKS 1167
<212> Type : PRT
<211> Length : 1167
SequenceName : SEQ ID 121
50 SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
55 <400> PreSequenceString :
MKTNGHFKDF AWKCKFLGAS VVALLVGCSP HIIETNEVAL KLVNHPASEK VQALDEKILL 60
LRPAFQYSDN IAKEYENKFK NQTTLKVEEI LQNGQYKVIN VDSSDKDDFS FAQKKEGYLA 120
VAMNGEIVLR PDPKRTIQKK SEPGLLFSTG LDKMEGV LIP AGFVKVTILE PMSGESLDSF 180
TMDLSELDIQ EKFLKTTHSS HSGGLVSTMV KGTDN SND AI KSALNKIFAS IMQEMDKKLT 240
60 QRNLESYQKD AKELKNKRRN 260
<212> Type : PRT
<211> Length : 260
SequenceName : SEQ ID 122
SequenceDescription :
65

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MKS K L K L K R Y L L F L P L L P L G T L S L A N T Y L L Q D H N T L T P Y T P F T T P L N G G L D V V R A A H L H P 60
S Y E L V D W K R V G D T K L V A L V R S A L V R V K F Q D T T S S D Q S N T N Q N A L S F D T Q E S Q K A L N G S Q S 120
5 G S S D T S G S N S Q D F A S Y V L I F K A A P R A T W V F E R K I K L A L P Y V K Q E S Q G S G D Q G S N G K G S L Y 180
K T L Q D L L V E Q P V T P Y T P N A G L A R V N G V A Q D T V H F G S G Q E S S W N S Q R S Q K G L K N N P G P K A V 240
T G F K L D K G R A Y R K L N E S W P V Y E P L D S T K E G K G D E S S W K N S E K T T A E N D A P L V G M V G S G A 300
A G S A S L Q G N G S N S S G L K S L L R S A P V S V P P S S T S N Q T L S L S N P A P V G P Q A V V S Q P A G G A T 360
A A V S V N R T A S D T A T F S K Y L N T A Q A L H Q M G V I V P G L E K W G G N N G T G V V A S R Q D A T S T N L P H 420
10 A A G A S Q T G L G T G S P R E P A L T A T S Q R A V T V V A G P L R A G N S S E T D A L P N V I T Q L Y H T S T A Q L 480
A Y L N G Q I V V M G S D R V P S L W Y W V V G E D Q E S G K A T W W A K T E L N W G T D K Q K Q F V E N Q L G F K D D 540
S N S D S K N S N L K A Q G L T Q P A Y L I A G L D V V A D H L V F A A F K A G A V G Y D M T T D S S A S T Y N Q A L A 600
W S T T A G L D S D G Y K A L G I V E N T A G L N G P I N G L F T L L D T F A Y V T P V S G M K G G S Q N N E E V Q T T Y 660
F V K S D Q K A T A K I A S L I N A S P L N S Y G D D G V T V F D A L G L N F N F K L N E E R L P S R T D Q L L V Y G I 720
15 V N E S E L K S A R E N A Q S T S D D N S N T K V K W T N T A S H Y L P V P Y Y Y S A N F P E A G N R R R A E Q R N G V 780
K I S T L E S Q A T D G F A N S L L N F G T G L K A G V D P A P V A R G H K P N Y S A V L L V R G G V V R L N F N P D T 840
D K L L D S T D K N S E P I S F S Y T P F G S A E S A V D L T T L K D V T Y I A E S G L W F Y T F D N G E K P T Y D G K 900
Q Q Q V K N R K G Y A V I T V S R T G I E F N E D A N T T T L S Q A P A A L A V Q N G I A S S Q D D L T G I L P L S D E 960
F S A V I T K D Q T W T G K V D I Y K N T N G L F E K D D Q L S E N V K R R D N G L V P I Y N E G I V D I W G R V D F A 1020
20 A N S V L Q A R N L T D K T V D E V I N N P D I L Q S F F K F T P A F D N Q R A M L V G E K T S D T T L T V K P K I E Y 1080
L D G N F Y G E D S K E A G I P L N I D F P S R I F A G F A A L P S W V I P V S V G S S V G I L L I L L I L G L G I G I 1140
P M Y K V R K L Q D S S F V D V F K K V D T L T T A V G S V Y K K I I T Q T S V I K K A P S A L K A A N N A A P K A P V 1200
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<212> Type : PRT
25 <211> Length : 1218
SequenceName : SEQ ID 123
SequenceDescription :

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<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
M H Q T K K T A L S K S T W I L I L T A T A S L A T G L T V V G H F T S T T T L K R Q Q F S Y T R P D E A L R H T N 60
A I N P R L T P W T Y R N T S F S S L P L T G E N P G A W A L V R D N S A K G I T A G S G S Q Q T T Y D P T R T E A A L 120
35 T A S T T F A L R R Y D L A G R A L Y D L D F S K L N P Q T P T R D Q T G Q I T F N P F G G F G L S G A A P Q Q W N E V 180
K N K V P V E V A Q D P S N P Y R F A V L L V P R S V V Y Y E Q L Q R G L G L P Q Q R T E S G Q N T S T T G A M F G L K 240
V K N A E A D T A K S E K L Q G A E A T G S S T T S G S G D T K V K A L K I E V K K K S D S E D N 300
G Q L Q L E K N D L A N A P I K R S E E S G Q S V Q L K A D D F G T A L S S S G S G G N S N P G S P T P W R P W L A T E 360
Q I H K D L P K W S A S I L I L Y D A P Y A R N R T A I D R V D H L D P K A M T A N Y P P S W R T P K W N H H G L W D W 420
40 K A R D V L L Q T T G F F N P R R H P E W F D G G Q T V A D N E K T G F D V D N S E N T K Q G F Q K E A D S D K S A P I 480
A L P F E A Y F A N I G N L T W F G Q A L L V F G G N G H V T K S A H T A P L S I G V F R V R Y N A T G T S A T V T G W 540
P Y A L L F S G M V N K Q T D G L K D L P F N N N R W F E Y V P R M A V A G A K F V G R E L V L A G T I T M G D T A T V 600
P R L L Y D E L E S N L N L V A Q G Q G L L R E D L Q L F T P Y G W A N R P D L P I G A W S S S S S S S H N A P Y Y F H 660
N N P D W Q D R P I Q N V V D A F I K P W E D K N G K D D A K Y I Y P Y R Y S G M W A W Q V Y N W S N K L T D Q P L S A 720
45 D F V N E N A Y Q P N S L F A A I L N P E L L A A L P D K V K Y G K E N E F A A N E Y E R F N Q K L T V A P T Q G T N W 780
S H F S P T L S R F S T G F N L V G S V L D Q V L D Y V P W I G N G Y R Y G N N H R G V D D I T A P Q T S A G S S S G I 840
S T N T S G S R S F L P T F S N I G V G L K A N V Q A T L G G S Q T M I T G G S P R R T L D Q A N L Q L W T G A G W R N 900
D K A S S G Q S D E N H T K F T S A T G M D Q Q G Q S G T S A G N P D S L K Q D N I S K S G D S L T T O D G N A I D Q Q 960
E A T N Y T N L P P N L T P T A D W P N A L S F T N K N N A Q R A Q L F L R G L L G S I P V L V N R S G S D S N K F Q A 1020
50 T D Q K W S Y T D L H S D Q T K L N L P A Y G E V N G L L N P A L V E T Y F G N T R A G G S G S N T T S S P G I G F K I 1080
P E Q N N D S K A T L I T P G L A W T P Q D V G N L V V S G T T V S F Q L G G W L V T F T D F V K P R A G Y L G L Q L T 1140
G L D A S D A T Q R A L I W A P R P W A A F R G S W V N R L G R V E S V W D L K G V W A D Q A Q S D S Q G S T T T A T R 1200
N A L P E H P N A L A F Q V S V V E A S A Y K P N T S S G Q T Q S T N S S P Y L H L V K P K K V T Q S D K L D D D L K N 1260
L L D P N Q V R T K L R Q S F G T D H S T Q P Q P Q S L K T T P P V F G T S S G N L S S V L S G G G A G G G S S G S G Q 1320
55 S G V D L S P V E K V S G W L V G Q L P S T S D G N T S S T N N L A P N T N T G N D V V G V G R L S E S N A A K M N D D 1380
V D G I V R T P L A E L L D G E G Q T A D T G P Q S V K F K S P D Q I D F N R L F T H P V T D L F D P V T M L V Y D Q Y 1440
I P L F I D I P A S V N P K M V R L K V L S F D T N E Q S L G L R L E F F K P D Q D T Q P N N N V Q V N P N N G D F L P 1500
L L T A S S Q G F Q T L F S P F N Q W P D Y V L P L A I T V P I V V I V L S V T L G L A I G I P M H K N K Q A L K A G F 1560
A L S N Q K V D V L T K A V G S V F K E I I N R T G I S Q A P K R L K Q T S A A K P G A P R P P V P K P G A P K P P V 1620
60 Q P P K K P A 1627
<212> Type : PRT
<211> Length : 1627
SequenceName : SEQ ID 124
SequenceDescription :

Sequence
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<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MGYKLLKRWPL VAFFTFTGIGL GVVLAACSAL NTSNLFPRQN RSKQLIGFTE NNIKPEAVL 60
KALAEDNGT ETILRVNFGE ALKSWYQNNK DRNIATRLTI FSENVEDEHD NLLDQKQAAE 120
5 PINWPIELQK EYDQWGGSES SWKALKLYDR LIADFQSLIF SNIVANVQLT DGSDQFKPTT 180
KDNLDSTSNK IKFVNSKPND PNGEFFANLQ AYLFAQWVVE ENPLPLTQAF FAYQAPKDGL 240
DSLYDQAAIG SALQLGYAFP AFREPNNQGS QGKTTFDPTP NSAQNFGDFI KAVFPEQKNG 300
QTQSSNTSSR TGLFDWQTKW NTNGAANKLL VTKSNLRGAF KGVGLATATII DQYEYLVGGS 360
KQSSQNDTFY QNQRKLSGGQ SGDNNSQGH HYLQDAVRLT SSQAMAAAST GADSSSGTNN 480
10 GGSSGGNSVL IPLPRSAALT HTQQQVQQTT STLQTPVYAR GDDGTALAI DGGDYFLANN 540
KRDFTKQADI LLYRYLQAKS NNFKENGVEF SLNLLSGLS FQTWAQTGLT AKLYGALVAM 600
MGSQGQTQVK GSVQGSRAA SVSQTTQQN RQSTDTQES EVVKLAKSL KSSADLAKPF 660
TDNPTFKKAL TDIQSEYKDY LAAAGKLSEF KKLGEVSGL QQAIIIDRADK YIQLEKQAQK 720
15 SAIGLQQLP YQRASDGSYP ALEKFFIPED SAADGKVKAS ESGSAALVTL KTTDSQKSTN 780
TVKQPDIKPT RENNDKKLKQ LTSDEVTKAS SLITKWGATP QIGSQFSEIV SLKSKDNKPQ 840
TMILALLSD VGIKWTKILN SFKEWFTNT NDFKNYDSE KKLKGNEYK DFNDLVKQTL 900
YLRWQRLTS KEKFGYKEL GSVKAQAAS GMVSLSSAA VANAVASSGM QKSGDQTLLE 960
LGKKAFFESL EASSSDGQYK YLRFLSTLMW LVKDGAKNYK RLLQQAITVG TRAFVSWTVS 1020
20 YDDTATASAA AKAQAVVLK TAQATNTQSD NPFNKVFQNP DYVQGSSETNW FNDKSTPIKP 1080
DSLLESESTY NFTAEPFDDK TKSQKRSTGG TTNEKHFFGF NGLTINSPOS VSTASAGLTE 1140
QIFNNFGQLV TSSDKSGALS QYKDKATLKR LIQNTNSDAE LNAFGEVLHR AVNVDTSNLG 1200
RPNSSGEPLI SFDNKKKFLV DVVDKLDVVY FNKFEGVVGQ TKVKMSDSSS SSQGTKTIRK 1260
PKPHHSRTR VSRLWMSFR LPRTLTKFL LVEKLIRTVL 1300
25 <212> Type : PRT
<211> Length : 1300
SequenceName : SEQ ID 125
SequenceDescription :
30 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MKKLLIKPQF WFLTLGGFIS SSVILVACAT PSNSALQTVF KARSNQFFNG EQGSLQNALA 60
35 TALKDPEANK QFVAAPLLKA LTAWYENNQD KQVTQFFKDT KKSVDQYNQ AVDKVVSASR 120
NKNLFVQQDL LDSAGGVRNL KSPEVVWTAH 150
<212> Type : PRT
<211> Length : 150
SequenceName : SEQ ID 126
SequenceDescription :
40 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MQQQGETKDQ YNTFGLRLVR NSVGVSVLGL DGFVKFIKGG SGGSNCGSSS AKKIDKEEQK 60
KFLKFRAPQA KIGTFYNTNF AFSFPLNETL KGWFDKHRGL ILANALVKVT LDTKEKASKA 120
LVDAFSSYKN WLSEYTPVGL ATTMISFYFD QMKALNNKLL ERVRSNLQNV NQANPTPWLN 180
GLSAKLPHYV TNGNYEKLNN YFTFLITKVL WPKVGTEDTN VSEKSKLKT KTEDVNKIRE 240
50 KILNNIDSKL KTFVQKLKPT LAPRPAYSNV ILLNINNDKV WSAGANWSLA VLLDPKKVNP 300
LSFMLLKQMF DQNSLFPKAK TLFENIQNKA KTSGSGKSGT TTNDADALS KVIGNYYYNT 360
WAKLTDKSIY GNLKDDKFDD LFKLAFDSSI NEKSFNVDYK AVIEHYRFYI TLEWLVDKNL 420
KNFKDLLKAN LKFGEIAFIA YKNTETQNF NPKGIFGSYF NYENETNAAK SATQIIDPNS 480
FFYKTTTKPE AKTTQSANTA VMVQNTQMN QQTNSYGFTE LSTSSGSM LG AATQQAILDQ 540
55 ITKTSLQQYG SQADLKKIIG ETKNQLLLDR IANQLIALKP NTSGNSGTQK TIAAYFQTD 600
VGNPTLDFKA KQKLLLDVLD QYKDFFGNNA QAVQRDSGKS GTGNYLTYTD GSDKITYLQF 660
SYKDIDGLSL SSSNGTSSKF ASDVVAALLL FQAAYKGTQ LALSSINKPQ LPIGDKRIKT 720
GIDLLK 726
<212> Type : PRT
60 <211> Length : 726
SequenceName : SEQ ID 127
SequenceDescription :
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65 <213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :

5 MKSFLRKPKF WLLLLGGLST SSIILSACAT PSNSALQAVF KPTSNQFFNG EHGTIQSALN 60
TALRDPEYNK KFVAAPLLKA LEAWYENNQD KNTIQFLKDT KTNVDNQYKT VVDKVVSAPR 120
NKSFLVQDDL LDSSGGSEAT WKARKLFEQL ISDFASRVFQ KNYLSYKENG KVSAGPFLYD 180
TISKNSNWQN IVFDAVNFPF TNDDFFAKIQ SEVFDQWAEY TDPTIISSVT LKYSAPN 237

10 <212> Type : PRT
<211> Length : 237
SequenceName : SEQ ID 128
SequenceDescription :

15 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :

20 MINFLFNQMN ALNNKFLERA KALNQNVNQA NPTPWLNGLS AKLPYVRTNG NYEKLNNYFT 60
FLIVKYMWK VGNEDASLSK DSSINKLTK TEDVNKIRDK ILEDIQKKVQ EFVKNKLKPT 120
LAPRQTYSNV ILLNVNNDKV WSMGANWALA NLLDTSKINP LSFMLLKQTF DQNDLFKKAK 180
KLFEDIQSKT NGSSSGGMQG SNTSSSEGAD ALSKVIGNY YNSWAKLTDK SIYGNPKDNK 240
FDDLFLKAFD DSINEKSFNV DYKAVIEHYR FIYLEWLVN GNLKNFKDLL KANLKFGEIA 300
FIAYKNTETK EFSNPQGVFG SAFNYENETN EVKIAAQNLD PNNFFYKTTT KPEEVKTAQN 360
GASMMVMQKN MQSTMQDSNH YGFTGLNTST SSMLGAATQQ ALLDQITKNS LQQYGSQQEL 420
KTLIEKTNQ LLLDRIASQL SGLNPSTTGN SNNKGKKNIA TYFQLDAIGN PTLSPQKQK 480
LLLDVLDQYK DFFGTNTQAA QRDGSGKGHG SYSTYQDQSD KITYLQFSYK DIDNLSLSDK 540
GNSKLASDVV AALLLFQAAD KGTQQLALSA IN 572

25 <212> Type : PRT
<211> Length : 572
SequenceName : SEQ ID 129
SequenceDescription :

30 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :

35 MKKFLRKPKF WLLTLGGFLS TSVILAACAT PSNSALQTVF KARSSQFFNG EQGSLQSALT 60
TALKNPVANK QFIAAPLLKA LEAWYENNED KKITQFLKDT KSNVDSQYTT AVDKVVSASR 120
NKSFLVQDDL LDNAGGSEAT WKAQKLLEQL ISDFASRVFQ KNYLNYKKDG QVSTGPFTYD 180
ELHKEESWKN MEFSAPRFSE TNDDFFAKIQ SQVFDQWVEY TDPTLISQVN YKYSAPSQGL 240
GQIYNREKLK DKLTPSYAFP FFAEEKDIAP NQNVGNKRWK QLVKGEGAIT DNNIGQSGTN 300
SQKTGLLKYR NESNKGDFLD PPLNLSDTNE TKQLVDASNI VDQLEAANLG AALNLKLQVF 360
EQDNDELPOI KELKEDLNNT IVVDKSKDVE KASKTNALFY NDQEGKQQQS DSDPIAGALD 420
DIFAFYFDQM KALNKLAEQV KKAATKMEA KTAVLRITNNS KGQNNYVVL DAAIPTFNST 480
TSKSKNNSAS NEVLVALKSG SINLRQVQQT DQNSYSPIKF RIVRNSTGVT VFGLDGGSY 540
LKQDSTNKS VSKQSLTLLT KSSSGNSNKV LRDLDKQKQF LKFRAPQAKT NTFYSTNFAF 600
SFPLNETLKS WFDKRELIL ANALVNASLD QKDKASKALT EAFNPYKELI KEFAPVALAT 660
TMISFYFDQM KALNKLKLER ARNLNQNVNQ ANPTPWLNGL SAKLPYVNTN GNYEKLNNYF 720
TFLITKTLPV KVGQEETSS EESNKLTKT ADVDKIRDKI LENIQTKVND FVKNKLKPAL 780
APRPAYSNVI LLNVNNDKVL SSGANWSLAS LLQSDKVNPL SFMLLKQAFD NNDLFKKAQK 840
LFKDIQEKSS NNGMQSSST TNSDADALSK VIGNYYTTW AKLTDKSIY NPKDNKFDEL 900
FKLAFASID EKSFNVDYKA VIDHYRFYT LQWLVDQKLE NFKSLKTNL KFGEVAFIAY 960

50 KNTETTNP SN PQGVFGSYFN YENSASEVKE STQTLDPNNF FYKTTTKPTV QAIQQVASLA 1020
LVQKQMQQN STDHYGFTGL STSTSSMFDA SSRDAILQOI TKTSLQYGS KDQLKKIIG 1080
TNNQLLLDRI AVQLSGLNPS TTNGGSGKTI ATYFQVDAVG NPTLDFQAKR KLLLDLLDQY 1140
QNYFGNGAQK SQRDSTPSGT GNYLTYQNGS DKYTYTQFTY QDIDSLSLTT TSGTNNKIAS 1200
DVVAALLLFQ AADKGTQQLA LSAINKPQLN IGDKRIESGL KLLK 1244

55 <212> Type : PRT
<211> Length : 1244
SequenceName : SEQ ID 130
SequenceDescription :

60 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :

65 MVGSGAAGSA SSLQNGSNS SGLKSLLRSA PVSVPSSSTS NQTLSSLNPA PVGPQAVVSQ 60
PAGGATAAVS VNRITASDTAT FSKYLNATAQ LHQMGGVIVPG LEKGGNGGT GVVASRRDAT 120
STNLPHAGA SQTGLGTGSP REPALTATSQ RAVTVVAGPL RAGNSSETDA LPNVITQLYH 180
TSTAQLAYLN GQIVVMSSAR VPSLWYWVG EDQESGKATW WAKTELNWGT DKQKQFVENQ 240

LGFKDDSNDS SKNSNLKTOG LTQPAYLIAG LDVVADHLVF AAFKAGAVGY DMTTDSNAST 300
 YNQALVWSTT AGLDSDGGTR LW 322
 <212> Type : PRT
 <211> Length : 322
 5 SequenceName : SEQ ID 131
 SequenceDescription :

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 10 <213> OrganismName : Mycoplasma pneumoniae
 <400> PreSequenceString :
 MPVFLKLTHT IRKVLRLVARL SRLALLSLTA VIFSGCANIN LISAVGSSSV QPLLKSLSSH 60
 YVLNHNDDKN LVEISVQAGG SSAGVKAITK GLADIGNVSK NTKSYAEENK QLWMDKKLKT 120
 ITLGKDAIAV IYKAPSEFKG KLVLTCKDNLN DLYDLFAGSK SVDINKFVEN GQTTKNSNHN 180
 15 LIGFPRITGA FASGTAEAFI KFSGLTQTKT LDKDSKEILE GQRNYGPNAR PTSETNIEAF 240
 NTFVTTLRQP NLYGMVYLSL GFVNMMNMLI KSEGFEVLKV KYDNNAVTPS SQAVSSNTYK 300
 WVRPLNSVVS LLPKQKTLPS IQRFFNWLLF SNNSEIKKIY DDFGVLELTA DEKKKMFKTG 360
 NAEMSNIANF WVDDYSLNNQ TFGAL 385
 <212> Type : PRT
 20 <211> Length : 385
 SequenceName : SEQ ID 132
 SequenceDescription :

 Sequence

 25 <213> OrganismName : Mycobacterium tuberculosis H37Rv
 <400> PreSequenceString :
 MSFAVLPPPEI NSARLYVGAG LAPMLDAAAA WDGLADELGS AAASFSAVTA GLAGSSWLGA 60
 ASTAMTGAAA PYLGWLSAAA AQAQQAATQT RLAAAAFEAA LAATVHPAII SANRALFVSL 120
 30 VVSNNLLGQNA PAIAATEAAY EQMWAQDVAA MFGYHAGASA AVSALTPFGQ ALPTVAGGGA 180
 LVSAAAAQVT TRVFRNLGLA NVGEGNVGNG NVGNFNLGSA NIGNGNIGSG NIGSSNIGFG 240
 NVGPGLTAAL NNIGFGNTGS NNIGFGNTGS NNIGFGNTGD GNRGIGLTGS GLLGFGGLNS 300
 GTGNIGLFNS GTGNVGIENS GTGNWIGENS GNSYNTGFGN SGDANTGFFN SGIANTGVGN 360
 AGNYNTGSYN PGNSNTGGFN MGQYNTGYLN SGNYNITGLN SGNVNTGAFI TGNFNNGFLW 420
 35 RGDHQGLIFG SPGFFNSTSA PSSGFFNSGA GSASGFLNSG ANNSGFFNSS SGAIGNSGLA 480
 NAGVLVSGVI NSGNTVSGLF NMSLVAITTP ALISGFNTTG SNMSGFFGGP PVFNLGLANR 540
 GVVNIGLGNAN IGNYNILGSG NVGDFNIGLS GNLGSQNLG SGNVGSFNIG SGNIGVFNVG 600
 SSGSLGNYNIG SGNLGIYNIG FGNVGDYNVG FGNAGDFNQG FANTGNNNIG FANTGNNNIG 660
 IGLSGDNQQG FNIASGWNSS TGNISGLFNSG TNNVGIENAG TGNVGIANSN TGNWIGINPG 720
 40 TDNTGILNAG SYNTGILNAG DFNTGFYNTG SYNTGGFNVG NTNTGNFNVG DTNTGSYNPG 780
 DTNTGFFNPG NVNTGAFDTG DFNNGFLVAG DNQGGIAIDL SVTTPFIPIN EQMVIDVHNV 840
 MTFGGNMITV TEASTVFPQT FYLSGLFFFG PVNLSASTLT VPTITLTIGG PTVTVPIISIV 900
 GALESRITTF LKIDPAPGIG NSTTNPSSGF FNSGTGTSN FQNVGGGSSG VWNISGLSSAI 960
 GNSGFQNLGS LQSGWANLGN SVSGFFNTST VNLSTPANVS GLNNIGTNLS GVFRGPTGTI 1020
 45 FNAGLANLGD IGNISANLGD FNLGSGNVGS FNVFSGNQGS YNIGPANLGN YNIGFANLGN 1080
 YNIGFGNAGD FNQGFANTGN NNIGFANTGN NNIGIGLSGD NQGGFNFAAG WNSGTANIGL 1140
 FNSGTNNVGI GNSGTGNWGI GNSGSGNTGI GNTGSTNTGF FNTGIVNTGV ANAGSYNTGW 1200
 YNTGDTNTGI ANLGDFNTGF YNTGNFSTGF ANQGDIAFGA FITGDMGNGA FWRGDQQLGF 1260
 SAGYRVHVPE IPAHVTVEVP VNIPITASFT NTVYSGITLE QINFGFTIDI AGIPLLAGAI 1320
 50 SKAVLPPIITG TGPATVNIIG DPGGSTAIRI PATASVGPFD VTFVNIAATT GFFNATTDPS 1380
 SGFFNGGPGT VSGIANIGAN ISGFQNVANS ATSGFNNGVS LQSGLANLGD TVSGVFNTGI 1440
 GAPANVSGMF NIGSNLAGFF HDQATGMSMF NLGLGNIGQF NVGFSNVGDS NAGLANIGSF 1500
 NLGSGNLGSF NVFNGNQGSY NIGPANLGN YNIGFANLGN NFGFGNAGDF NLGFANTGNN 1560
 NIGFANTGNN NIGIGLSGDN QQGFNFAGGW NSGSGNSGLF NSGTNNIGLF NSGTGNIGIG 1620
 55 NSGTGNWGIA NTGDTNTGIF NTGDNVTGLL NAGNVNTGIF NTGHYNTGSF NAGSFNTAGF 1680
 NPGSYNTGYL NTGSYNTGLA NSGDVNTGGF ITGNYSNGFW WRGDYQQLAG ISQITITVPDT 1740
 AVPVKLHVPI FLDIPVTGTL GTFTVHGFRF PEITGDIFLI GIPFNAATLD AFSFNPISIV 1800
 LPNIGINLGS GPDPIDIDAG TGGLLEPIKIP LIDIPAAPGF GNSTTTPSSG FFNAGTGTVS 1860
 GGVNVGSNSS GFFNLTSGLS GISGVQNFGE LISGGFNFCN TVSGLVNST LGLSMPANLS 1920
 60 GGNVGATVA GFVNNTQILN LGFNVGSGN VGHGNIGDSN VGLGNLGNAN VGHGNIGSFN 1980
 VFGNNGRSYN IGLPANLGN YNIGFANLGN LGFANSGSNN IGFANTGNN 2040
 IGLGLSGHNQ QGFGSWNSGT ANTGLFNSGT NNIGLFNSGT GNIGIGNSGI GNTGIGNPGV 2100
 GNTGLGNSGT GNWGLWNPST GNMGVANVGT YNTGGYNVGS TNTGIANVGI ANTGSYNTGS 2160
 TNTGSFNDGD FNTGFYNTGD YNTGFYNTGD VNTGAFIIGN FSNGAFWQSD HQGQWGAHYA 2220
 65 ITVPQIPLLN IGLNIPVNI IHLDFGTILAV NGFQIPATL RALGVTHFSV GPIIVPRIAG 2280
 TLPVIDINIG DPGGSSSIPI TITSGAGPVV IPLLIDIPAP GFGNSTTGPS SGFFNSGTGS 2340
 SSGFGNVGAN NSGFWNATAF GIGNSGLQNF GSLQSGWANL GNTVSGFYNT SAADFATPAN 2400

	LSGLSNVSGAD	LTGVLRGPNG	STFNAGLANL	GQFNVGSA NL	GSANLGSANL	GSANLGNSNV	2460
	GFGNIGNANI	GGANIGDFNV	GIANTGPGLT	AAVNNIGIGN	TGNYNIGVGN	TGNYNIGFGN	2520
	TGNNNIGIGL	SGDNQIGFGP	LNAGIANMGL	FNLGDNNGFM	ANAGNFNQGI	ANTGNNNIGL	2580
	FNTGNNNVGI	WLTGDLGSGF	SSLNSGAGNT	GFFNSGTANT	GLFNSGTGNT	GLFNSGTGNV	2640
5	GIGNMTGGF	GVGLSGDSQV	GIGGTNSGSF	NIGLFNSGTG	NVGIGNSGTG	NVGIGNGTGTG	2700
	NTGIGNSGNY	NTGLLNAGLV	NTGIANPGNH	NTGLFNIGTF	NTGIANPGHY	NTGSYNTGSY	2760
	NTGMANAGDY	GTGAFITGSM	NNGLLWRADR	QGLLAANYTI	TIERPAAFLN	VDIPVNIPIT	2820
	GDITNVSIPA	ITFPRIDASG	SVDIGILSGT	VLAPVGPITL	HGGDASAPLD	TPIEIDFGPS	2880
	PAINLNICKP	DGSTVINIVG	GAGAGPISIP	IIDLRPAPGF	FNATTGPSSG	FLNHWAGSAS	2940
10	GLLNFGNNSY	LYNFATSSMG	NSGFQNYGSL	QSGWANLGNS	ISGIYNTGLG	APANVSGLLN	3000
	IGTNLAGWLQ	NGPTETTFSV	GLANLGFWNL	GSANIGNYNL	GSANIGVYNL	GSANIGDFNL	3060
	GSANIGDFNL	GSANIGSSNI	GFCNVGPGLT	AAIGNIGFGN	TGNGNIGIGN	TGTGNIGFGN	3120
	TGNGNIGIGL	TGDTMTGFGG	WNSGTGNIGL	FNSGTGNIGF	GNSGTGNWGI	GNSGDYNTGI	3180
	GNTGSTNSGF	FNTGLVNTGI	GNSGDYNTGL	FNAGNTNTGS	FNPGDYNTGG	FNPGNYNTGY	3240
15	FNPGNSNTGI	ANSQDVNTGA	FNSGNYSNGF	FWRGDYQGLG	GFAYQSAVSE	IPWSYDRFQH	3300

<212> Type : PRT

<211> Length : 3300

SequenceName : SEQ ID 133

20 SequenceDescription :

Sequence

	<213> OrganismName : Mycobacterium tuberculosis H37Rv	
25	<400> PreSequenceString :	
	MNLVSTTSGM SGFLNVGALG SGVANVGNTI SGIYNVGTSD LSTPAVNSSL ANIGTNIAGL	60
	LRDGAGTAAI NLGLANHGNI NVGFASLGGF NFGGATIGHN NVGIGNTGIF DVGLANLGSY	120
	NIGFGNLGDD NLGFGNFGSY NIGFNVGND NLGFANAGGG NIGFANTGSN NVGFGNTGSN	180
	NVGIGLTGNG QIGFGSFNSG SGNIGLFNSG SNNIGFNSG SGNFGIANSN SFNTGIGNTG	240
30	NTNTGLFNSG DVNTGAFNPG SFNTGSFNTG SFNTGGFNPG NTNTGYLNIG NYNTGIANTG	300
	DVDTGAFITG NYSNGLFLSG DYQGLVGLNL VIDMPLPISL GVNIPIDIPI TASAGNITLM	360
	GVTIPPTGDI VLSSIAGQRA HFGPITIPNI TVVGPTTTVA IGGPNTAITI TGGGAIRIPL	420
	ISIPAAPGFG NSTTNPSSGF FNTGAGGASG FGNFGGANSN FWNLASATSG ASGLLNVLGAL	480
	GSGLANVGTT VSGFYNTSTS DLATPAFNNG LANISTSIAG LLRDSTGTMTV LNLGLANHGT	540
35	LNVGIANLGD YNIGFANLGS ANFGSANIGG NNIGGANTGI FDIGLANLGS YNIGFGNFGD	600
	DNLGFGNLGS YNVGFGNLGN DNLGFANTGS NNIGFANTGS NNIGIGLTGD GQIGFGSLNS	660
	GSNGIGLFGN GSGNIGFPNS GNGNVGIGNT GTANFGGLNT GSTNTGFFNS GDVNTGIGNT	720
	GSFNTGSFNP GDSNTGDFNP GSYNTGLGNT GDVDTGAFIS GSYNNGFLWS GNYQGLIGLH	780
	AALAIPEIAL TFGVDIPIHI PINIDAGVVT LQGFSSIVAAE NNIDFTPIII PTINITLPTA	840
40	AITVGGPTTS IGITASAGIG SITIPIDIP ATSGFGNSTT SPSSGFFNSG AGSASGFLNV	900
	VAGASGIFGV LNVGALGSGV TNVGHTVSGF YNASALDLVT PAFASGLMRD GMGMTLNLG	960
	LANLGSNNAG FNGTGIFDVG VANLGNYNIG FGNFGDDNLG FANLGSYNIG VANTGSNNIG	1020
	FANTGSNNIG IGLTGTGQIG IGAALNSGSGN IGLFNSGDGN IGGFNSGTGN FGIANTGTGN	1080
	FGIGNSGSTS TGLFNSGDGN TGGFNPGNFN TGNFNTGSFN TGGFNAGNTN TGHFNTGNYN	1140
45	TGIANTGDVS TGAFISGNYS NGILWRGDYQ GLIGYSYALT IPEIPALHDV NIPIDIPITG	1200
	SFTDLVVDFN TIPIIGFESF AFSFHIHTEP DIGPIIVPSF VLSVPTFAIA VGGPTTAINI	1260
	SATAGLGPIT IPIIDIPAAP GIGNSTTSPS SGFFNTGAGT ASGFGNVGGN TSGLWNLASA	1320
	ASGVSGLLNV GALGSGVANV GNTISGIYNT SPLDLGTPAF GSGLANIAGL LQGGAGTTIL	1380
	DLAGLGNLNV GLANLGGSNF GIGNTGIFNV GFANVGNHNI GLANLGNYSV GFANSGNYHI	1440
50	GIANTGSANI GFANTGSGNI GIGLTGTGQI GFGSFNSGSH NIGLFNSGDG NVGFFNSGTG	1500
	NVGIGNTGTA NFGIANSNGS NTGLGNTGST NTGLFNPGNV NTGVGNTGSI NTGSINTGSF	1560
	NTGSTNTGSF NLGDHNTGSF NSGDYNTGYF NAGDYNTGVA NTGNVNTGAF ISGNYSNGFF	1620
	WRGDYQGLIG LSTTITIPET PYRYDLSVPI DIPITGTVVA TTPNSFTIPG FQIRVLLGPA	1680
	AVLVNEMIGP ITIDVNQVIA IDSPIQQTIS MVGTGGFGPI PIGISIGGTP GFGNSTTGPS	1740
55	SGFFHTGAGH VSGFGNFGAG NMSGSGNFGA GNSGFFNAGG LGNSGLLNFG ALQSGLANLG	1800
	NTISGVYNTS TLDLATPAFG SGIANIGANL AGLFLDNTGN LTLNFGVANQ GGLNAGIGNL	1860
	GSVNIGFVNT GDSNLGIGNL GDLNFGGVNI GGNNGIANT GIFDIGLANL GSYNIGLANL	1920
	GDDNLGFGNA GSYNIGFANF GSDNLGFANT GSYNIGFANT GNNNIGVGLT GNGQIGIGSL	1980
	NSGSNNIGLF NSGSGNIGFF NSGTGNVGIF NTGTGNFGLA NSGGFNTGIG NAGSTNTGVF	2040
60	NPGLDNTGSF NPGSFNTGGF NPGSGNTGYL NTGDYNTGVA NTGDVDTGAF ITGSYSNGFL	2100
	VSGDYQGLIG LPLLGPVTP GYFNLTGGPS SGFFNNSGAGS VSGFVNSGAG LSGYLNLTAL	2160
	SGSVANVGNT ISGWLNASAL DLATPGFLSG IGNFNGTNLAG FFRG	2204

<212> Type : PRT

<211> Length : 2204

65 SequenceName : SEQ ID 134

SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv

<400> PreSequenceString :

5	MSFVLIAP	EF	VTAAAGDLTN	LGSSISAANA	SAASATTQVL	AAGADEVSAR	IAALFGGFGL	60
	EYQAISAQVA	AYHQR	FVQAL	STGAGAYASA	EAAAAEQIVL	GVINAPTQAL	LGRPLIGDGA	120
	NATTPGGAGC	AGGLLF	FGNGG	AGAAGAPGQA	GGPGGPAGLW	GNGGPGGAGG	SGGGTGGAGG	180
	AGGWLF	GVGG	AGGVGGAGGG	TGGAGGPGGL	IWGGGGAGGV	GGAGGGTGA	GGRAELLFGA	240
	GGAGGAGTDG	GPAT	TGGTGG	HGGVGGDGGW	LAPGGAGGAG	GQGGAGGAGS	DGGALGGTGG	300
10	TGGTGGAGGA	GGRGALLLGA	GGQGGGAGG	QGGGTGGAGG	DGVLGGVGGT	GGKGGVGGVA		360
	GLGGAGGAAG	QLFSAGGAAG	AVGVGGTGGQ	GGAGGAGAAG	ADAPASTGLT	GGTGFAGGAG		420
	GVGGQGGNAI	AGGINGS	GGGAG	GGTGGQGGAG	GMGSGADNA	SGIGADGGAG	GTGGNAGAGG	480
	AGGAAGTGGT	GGVGAAGKA	GIGGTGGQGG	AGGAGSAGTD	ATATGATGTT	GFSGGAGGAG		540
	GAGGNTGGVGG	TNGSGGQGGT	GGAGCAGGAG	GVGADNPTGI	GGTGGTGGKG	GAGGAGCQGG		600
15	SSGAGGTNGS	GGAGGTGGQG	GAGGAGGAGA	DNPTGIGGAG	GTGGTGGAAAG	AGGAGGAI	GT	660
	GGTGGAVGSV	GNAGTGGTGG	TGGVGGAGGA	GA	AAAAAGSSA	TGGAGFAGGA	GGEAGGAGNS	720
	GVGGTNGSGG	AGGAGGKGCT	GGAGGSGADN	PTGAGFAGGA	GGTGGAAAGAG	GAGGATGTGG		780
	TGGVVGATGS	AGTGGAGGRG	GDGGDGASGL	GLGLSGFDGG	QGGQGGAGGS	AGAGGINGAG		840
	GAGGNGGDDG	DGATGAAGLG	DNGGVGGDGG	AGGAAGNNGN	AGVGLTAKAG	DGGAAGNNGN		900
20	GGAGGAGGAG	DNNFNGGQGG	AGGQGGQGGG	GGASTTSINA	NGGAGGNGGT	GGKGGAGGAG		960
	TLGVGGSGGT	GGDGGDAGSG	GGGGFAGGAAG	KAGGGGNGGR	GGDGGDGASG	LGLGLSGFDG		1020
	QGGQGGGAGG	SAGAGGINGA	GGAGGNGDGG	GDGATGAAGL	GDNGGVGGDG	GAGGAAGNNG		1080
	NAGVGLTAKA	GDGGAAGNNG	NGGAGGAGGA	GDNNFNGGQGG	GAGGQGGQGG	LGGASTTSIN		1140
	ANGGAGGNGG	TGGKGGAGGA	GT	LVGGSSGG	TGGDGGDAGS	GGGGGFGGAA	GKAGGGGNGG	1200
25	VGGVGGEGAS	GLGLGLSGFD	GGQGGQGGAG	GSAGAGGING	AGGAGGTGGA	GGDGAPATLI		1260
	GGPDGGDGGQ	GGIGGGGNA	GFGAGVPDGG	GDGGNAGFGA	GVPDGGGIGG	TGGAGGAGGA		1320
	GADGDP	PSIDG	QGGGAGGHGG	QGGKGG	LNST	GLASA	SGDGG	1380
	GS	GGTGGTGG	DAGVGG	LANT	GGTGGTGG	NAGIGGAGGR		1440
	QGGVGGNAGA	GGINGAGGTG	GTGGAGGDGG	NGTTGVASEG	GAGGQGGDGG	QGGIGGAGGN		1500
30	AGFGAGVPGD	GGIGGTGGAG	GAGGAGADGD	PSIDGGQGGG	GGHGGQGGKG	GLNSTGLASA		1560
	ASGDGGNGGA	GGAGGNGDGG	DGFTGGSGGT	GGTGGDAGVG	GLANTGGTAG	NAGIGGAGGR		1620
	GGDGGAGDSG	ALSQDNGNFA	GGQGGQGGVG	GNAGAGGING	AGGTGGTGGG	GGDGGQNGTTG		1680
	VAGGAGGAGQ	GGDGGQGGIG	GAGGNAGFGA	GVPGDGGTGG	TGGAGGAGGA	GADGDP	PSIDG	1740
	QGGGAGGHGG	QGGKGG	LNST	GLASA	SGDGG	GGTGGTNGNG		1800
35	GLGGGGGNGG	AGGAGGTPTG	SGTEGTGGDG	GDAGAGGNGG	SATGVGNGGN	GGDGGNGGDDG		1860
	GNGAPGGFGG	GAGAGGLGGS	GAGGGTGDGD	GNGGSPGTGG	S			1901

<212> Type : PRT

<211> Length : 1901

SequenceName : SEQ ID 135

SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv

<400> PreSequenceString :

45	MSLVIVAPET	VAAAAALDVAR	IGSSIGAANA	AAAGSTTSVL	AAGADEVSAA	IATLFGSHAR	60	
	EYQAISTQVA	AFHDFRAQTL	SAAVGSYVSA	EATNAAPLAT	LEHNVNLNALN	APTQALLGRP	120	
	LIGDGAAGAP	GTGQAGGAGG	ILWNGNGAGG	SGAPGQVGGG	GGAAGLFGTG	GAGGAGGAGA	180	
	AGGAGGSGGW	LLGNGGVGGA	GGQSLGGAT	GGAGGNAGLF	GVGGTGGPGG	PGGPGGVGGT	240	
50	GGAGGLGCTL	YGAGGHGGAG	GP	PIGGVGG	HGGVGGAGL	LVGGHGGAG	GHGAEVAGA	300
	AGEDLSPHGT	SGGVGGDAGD	GGTGGRGWL	AGAGGAGGAG	GVGGTGGAGG	AGFSRALIVA	360	
	GDNGGDPGAG	GAGGTGGAGS	TIGAHGAAGA	SPTSGGNGGA	GGNGAHFSSG	GKAGGNGGAG	420	
	GAGGLVNGG	AGGAGNGAP	GAPPSGGDPN	GGGGGAGGAG	GKGGDGGQA	GDGGAGGAGG	480	
	KGGNGNGAT	GATGLNGLGA	GADGTDGGKG	GNGGAGGGGG	AGGQGGKALA	ATHQDGSMA	540	
55	GGAGCNGGAG	GMGGDGGNGA	KGTFDNGGDG	VGGNGGNGGS	RGIGGAGGIG	GAGSTAGADG	600	
	ARGATPTSGG	NGGTGGNGAN	ATVAGGAGGA	GKGGNGGLV	GNGGAGGKGG	DGMAGVAGSS	660	
	PTTAGESGTS	QNGGAGGAG	GAGGRGGDFG	GDGGTGGAGG	NGANGANATT	PGAKGGDGGH	720	
	GGPGAQGGNG	GQGGPGGLAG	NLFGQNGIQG	VGGSGGKGGG	GGLAGDGGNG	ANGNFAGDGG	780	
	NGGHGNGGN	PGAGGQGGSG	GAGSTPGAKG	AHGFTPTSGG	DGGDGGNGGN	SQVVGNGGGD	840	
60	GGNGGNGGSA	GTGGNGGRGG	DGAFGGMSAN	ATNPGENGPN	GNPGGNGGAG	GAGGAGLNGG	900	
	NGGAGGNGGL	GGFGNGAAG	ANGVAVGAPG	QPGGAGGHGG	AGGNGGAGGN	GGQGVVSDGA	960	
	GGAGGAGGDC	GAPGDGANGG	NGQAGAFAG	GGGGRGGDGG	NAGNAGAGGP	GGTGSTAGKA	1020	
	GPAGSILHDG	GNGGHGGHGA	ASGNGGGPGG	HGGNGGNGGT	GANGGNGGIG	GTGGAGSTGA	1080	
	KGVLTGNEGD	GGDGGRGNG	GRGNGGGQGL	TCAGGNGGTG	GTPGNGGNGG	NGASGDLVTS	1140	
65	PGDGGGGGRG	GCDGGRGGDAG	LGGSSGPGGT	PGDWTGTTGT	GTGGTGGQGA	NGGLTGGRGG	1200	
	TGGNGGNGNT	GGTGGAGGTG	GTGHNGSQPG	MGGNGGAGGF	GGNGFAGVGG	RGGMGGSGGT	1260	
	GCTGDAGPFG	TGTGGTGGHG	GQGGGGGFSI	LLGLGGLGGL	GSPGSIATGT	AGGAGGGGGF	1320	

GGGCGGEFV 1329
<212> Type : PRT
<211> Length : 1329
SequenceName : SEQ ID 136
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

10 MSYVIATPEM MATAAFDLAR IGSQVSAASA VAAMPTTEVV AAGADEVSAG IAALFSAHAQ 60
EYQALSAQAA AFHDQFVHTL TAAARWYTAT EIANAAAMRV VLGAVNAPTQ TLLGRPLIGD 120
GAHGTAAPGP GGAGGLLFGN GGNGAAGAVG QVCGAGGAAG LFGIGGAGGA GGAGAPGGTG 180
GTGGWLAGGG GVGGMGGAGG GAGGAGGNAG LFGNGGAGGA GGAGGGAGGA GGNAGWFGHG 240
15 GAGGVGGVGA AGANGATPGQ DGAAGVAGSD DGAGCDGLAG SDGGDGGAGG VGGNGGRGGW 300
LLGNGGAGGV GGVGGAGGAG AAGGAGGAGA TGINGPAGIS AAGDDGGAGG NGGAGGNGGV 360
GGAGGAGGSA GLLGYVVRAG DGGAGGGGGL GGAFCDDGAG GNGGSWLAAG DGGAGGHGGD 420
PGLGGAGGAG GASGGAGARA GANGLAAGND GPVSGGNGGK GNGGAHAPVA GGHGNGGGAG 480
GNGGLVGDGG AGGHGGDGA GAGYADMTAI FLGSSGTPGE DGGNGGAGGA GGAGGAHAGD 540
20 GGAGGAGGNG GAGGAGGNGA HGFNAVLVSD GNGGDDGGAG GRGGDGGAGG AGGDAPAGRA 600
GSQGVGGDGG AGGAGGAPGN GSGGGRGDMA FKDDGGAGG DGGDPGAGGK GGAGGAGATE 660
GVTGATGATV HSGGNGGKGG NGADATVAGA NGGKGGAGGN GGLVGDGGAG GDGSGAAGA 720
NGANVGEDGA DGTLSGQPGG GSEANGGQGG VGGGGAGGAG GDGGAGSSAL GSGGNGGRGD 780
AGQAGGAGGA GGAGGAGGSV SGDGGPGGKG GAGGAGGAGA SGGGGKKGAS GADSAEAVGG 840
25 AGGKGDDGGV GGVGGDGGPG GDGGAGGAAP AGQVSGHVG GVGDDGGLGG AGGNGDGGH 900
GSDGGDGGDG GDFGAGGLGG LGGDSGNGTR AASGVDASDH GPGSGGNGGN GGNGAASVA 960
GGAGGNGGDD GNAGRVGDGG AGGNGGDGAA GANANGSAP GSDALALGQP GNGGQGDAG 1020
QAGGAGGAGG AGGAGGSVSG DGGAGGNGGA GNGGCVGASG GAGARGANGI DSIGGTGGAG 1080
GGGDDGGAGG VGGHGGDGGV GGAAPSGTVG SHGTGGVGGD GGLGGAGGVG GAGGNGGIGI 1140
30 TVGGAGGAGG NGGDPGAGGR GGLGGDSGNG TSAANGVDAS KHGPLTGGDG GVGNGAKAA 1200
AAGDDGGQGG DGGNAGLFGD GGAGGDGADG TAAEALGGDG GAGGAGGKGG DAGDIGDGGD 1260
GGKGGDGAHG ALGGLTVAGG NGGAGGAGGA GGAGGAFLGD GNGGAGGQGG GAGRGSGPGG 1320
GGGNGGAGGA GGDAGMNGGG GTGGQGGNGA AGGAGWSPDS DLKGFDFDGG GSGGAGDGG 1380
AGGAGGTQTG DGGDGGAGGL GGAGGVGGNG VDFDINETT GRDGGDGGDG GYGGWGGAGG 1440
35 NGGAGGSAPA GEVGNRGVGG DGGDGGSGGD AGNGGLGGDG FTYLADFDGE PGDDGGDGGD 1500
GGWRPGGQG GFGSTSGAHG KAGFGAPGGD GGDGNGGHHG GDGNGSFADA GDGPGGNGG 1560
NGLGGAGARD GGAPGGDGGD GGTGSGGGFG APPRSIGGG DGGDGGRGD GGRGAGGLTS 1620
GGVSSGESG GSGNGRGDPG SGGSGGEGGE GGPSSISVNV 1660
<212> Type : PRT
<211> Length : 1660
SequenceName : SEQ ID 137
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

45 MSFVLVSPET VAAVATDLKR IGASLAHENA SAAASTTAVV SAAADEVSTA VAALFSQHAQ 60
GYQAAAQVA AFHSRFVQAL TAGAGAYafa EAANASPLQS AMGAVSASAQ TLLSRPLIGN 120
50 GANATTTPGGN GGDGGWLFGS GGNGAPCAAG QSGGNGGSAG LWNGGAGGA GSGGAAGGN 180
GGNGGWLFGA GGTGGIGGTG APGAMGGTGG NGNGALLIG GGGLGGAGGM GGTGGGTGGT 240
GGNGGNGALL IGAGGVGGAG GIGGQGTGAG GAAGAGGTGG NGGAGGLFMN GGDGGAGGQG 300
GDGAAGDAAA SAGGTGGKGG QGGDGGTGGA GGAGPVLFGH GGAGGMGGQG GTGGMGGAGG 360
DGTTVIAAGT GEGGTTGGAA GAGGAAGARG ALTSGGLAGG VGAGGTGGTG GTGNGADAA 420
55 AVVGFANGD PGFAGGKGN GGIGGAAVTG GVAGDGGTGG KGGTGGAGGA GNDAGSTGNP 480
GGKGGDGGIG GAGGAGGAAG TGNGGHAGNT GDGGDGGTGG NGNGTGGVN GADNTLNPDT 540
PGGAGEPPGA GGAGGAGGAA GPGGTGGTG GNGGNGNGG NGGNGNGGN GGNAGNNSTN 600
APVGGEGGAG GDGGAGGAG AANGTAGSQ GTGGVGGDGG AGGNGGKKA GTGNSGNFGV 660
DGEAGFSGGA GNGGCVGGA GANGTGGS GNGGDDGAGG IGGAGNGIP GTGTEPAGGT 720
60 GAKGGDGGDG GAGGAGGNAG GAGGQGNAG QGGAGGAGGN AVIPGDGVGK APHGAGGSG 780
GDGGKGGQGG SGGTGGSGAP IGGAGGTGG SGHAGKGA GGIGAQTII TVPNGNGAG 840
DGGNGGAGG GNGGSGDFG GNTTSGASGS GNGGNGAGTA GSGGAGGTGG TGLSGGNGN 900
GGNGGNGDG GNGAHGTGVA QFVPATSLPT PNGGAGNGG TGSNGGAPGP AGAPGPTTGG 960
NAGSQIGGD GNGGDDGGKG GDGADAVNVV FMPTEPQAAT GTAGSAGDPT GNGGPGPTPG 1020
65 SPMVAPPPT PITQVQGGD GGAGGTGSTN ANDGTATGK GEGGVGSIL GPGGNGGTG 1080
GNASATGTNG VANGNGGKG GDGGQFGAGG NGGAGGSVTD GSAGSTAGNG GNGGNATNGT 1140
IAGQPAGGNG SAGGKGGDGG NIAAGATGTA GNGGNGGNGN DGAVNAGTGG SGGNGGAGG 1200

GGANGGDGGA GGAGGAGGRG KGKIDGGFGG DGGNGGSNNG TGAGGNGGNG GTGGVGSVGA 1260
AGGDGNGGGT GGFAGFGGTA GNGGSGGTGG AGGDGGTGGD GGNGVIAGGG GTGGNGGASG 1320
AGGAGGTGGF AGNGNAGGNG GTGGASEDGD NGNAGSGATG GTGGNGGTGG DGGAAAGLGGV 1380
A 1381

5 <212> Type : PRT
<211> Length : 1381
SequenceName : SEQ ID 138
SequenceDescription :

10 Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVIATPEM LTTAATDLAK IGSTITAANT AAAAVAKVLP ASADEVSVAV AALFGTHAQE 60
15 YQTVSAQVAT FHDRFVQTLA AAASSYVAEE AVNVEQSLLA AVNAPTQALF GRPLIGNGAD 120
GSPGTGQAGG PGGILYGNNG NGGSGAPGQR GGAGGAAGLI GNGGNGGAGG VGTGTGAGGH 180
GGAGGWLYGN GGAGGFGGAG AVGGNGGAGG TAGLFGVGGG GGAGGNGIAG VTGTSASTPG 240
GSGTAGGAGG IGGNGGAGGA GGVLMGNGGN GGAGGEGGPG GAGGAGASGA HATNLGADGQ 300
AGGNGGNGGA GGTGGVGGPG GGHLLGLGG SHGAGCAGGS GGDGAPGDG GNGATGTWGH 360
20 NLGAGGTGGN GGNPAGGAG GAGGASVGGG AHGANGAPGT TSTSGGNGGD GKGADAISS 420
GQTGANGGRG GDGGQVGNNG AGGAGGRGGA GGLFGGSEAP GRPGGAGGT GAGNGGTQA 480
GDGGTGGAGG AGGDGSGGA GSIGFNASAP GAAGSPGGNG GNGGPGGAGG EGGAGGLALA 540
ASGQNGSQGA GGDGAGGNG GTPGNGGHA AGALGVNNGV GGAGGHGGDP GVGAGGQGG 600
SGSTPGANGA PGNPTSGGN GNGGGRGADA TGFQGTGASG GRGGDGLVG NGGAGGAGGN 660
25 GSKGLPGLGR LGNPGLDGGT GNGGAGGSG GAWAGNGGTG GAGGTGGVGG TGGSGSDGVN 720
GSSAGADGHP GGTGGVGGTG KGKGDGGDGG AAPNVAGSQ GPGGAGGDGG TGGVGNNGGR 780
GIDGADGATA GARGQDGGAG GAGGKGRGG TGGPGGAGPA GTGSGQAGG NGGSGGTGGD 840
PGDGGNGANG SVFTNNGIGG NGGNGGNAGP SGAGGSGGAG STFGATGSSS SIHVNGGNGG 900
NGGNGDHALS GNGAAGGNG NGGNGSLRGS GGAGGHGNG GNASRCMGD GGTGAGGNA 960
30 GQIGNGAGG NGGDGGTSD GNPGAITGSG GRGGDGGVGG QGGSVAGDGA DGGRGAGGT 1020
GGTGLRGTG ATGATGTFDA GADGHGNGG TGGVGGTGA GGGGNGGAG GKALSPTGNN 1080
GSQAGGDDG AGGAGGTGGT GGDGGRGAGH TLFSSLAGTG GTGGNGGTGG TGGTGGAGGA 1140
GGTGSTLGAT GATGAAGRAG NGGVGSGGGL GSAPGPGGT GMGGAGGTST VSAGDGGRG 1200
GFGGGLDAS SGGNGDGGH GGDGFRTAGA GGRGGDGGK ADPGGLFPIP GAGGKGGTGG 1260
35 TGCTAHLGPL AIIGQSGQPG QFGSPGADGR GGAGGAGGGG GAGGSF 1306
<212> Type : PRT
<211> Length : 1306
SequenceName : SEQ ID 139
SequenceDescription :

40 Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
45 MSAAVAWDQ LAMELASAAA SFNSVTSGLV GESWLGPSSA AMAAAVAPYL GWLAAAAQA 60
QRSATQAAAL VAEFEAVRAA MVQPALVAAN RSDLVSLVFS NFFGQNAPI AAIEAAYEQM 120
WAIDVSVMSA YHAGASAVAS ALTPFTAPPQ NLTDLPQALA AAPAAVVTAA ITSSKGVLAN 180
LSLGLANSFG GQMGAAANLGI LNLGSLNPGG NNFGGLNVGS NNVLGNTGN GNIGFGNTGN 240
GNIGFGLTGD NQQFGGWNS GTGNIGLFNS GTGNIGIGNT GTGNFGIGNS GTSYNTGIGN 300
50 TQANTGFFN AGIANTGIGN TGNNTGFSN LGSFNTGDFN TGSSNTGFFN PGNLNTGVGN 360
TGNVNTGGFN SGNYSNGFFW RGDYQCLIGF SGTLTTPAAG LDLNGLGSVG PITIPSITIP 420
EIGLGINSSG ALVGPINVP ITVPAIGLGI NSTGALVGPI NIPPITLNSI GLELSAFQVI 480
NVGSISIPAS PLAIGLFGVN PTVGSIGPGS ISIQLGTPPI PAIPPFPPGF PPDYVTVSGQ 540
IGPITFLSGG YSLPAIPLGI DVGGGLGPFT VFPDGYSLPA IPLGIDVGGG LGPFTVFPDG 600
55 YSLPAIPLGI DVGGGLGPFT VFPDGYSLPA IPLGIDVGA IGPLTTPPI IPSIPLGIDV 660
SGSLGPINIP IETAGTPGFG NSTTTPSSGF FNSGTGTSF FGNVSGSGSG FWNIAAGNLN 720
SGFLNVGPLT SGILNFGNTV SGLYNTSTLG LATSAPHSGV GNTDSQLAGF MRNAAGGTLF 780
NFGFANDGTL NLGNANLGDY NVGSGNVGSY NFGSGNIGNG SFGFGNIGSN NFGFGNVGSN 840
NLGFANTGPG LTELHNIGF GNIGGNNGYF ANIGNGNIGF GNTGTGNIGI GLTGDNQVGF 900
60 GALNSGSGNI GFNSGNGNI GFNSGNGNV GIGNSGNYNT GLGNVGNANT GLFNTGNVNT 960
GIGNAGSYNT GSYNAGDTNT GDLNPGNANT GYLNLGDLNT GWGNIGDLNT GALISGSYSN 1020
GILWRGDDYQ LIGYSDTLGI PALPLSVEVN GGIGPIVVPD ITIPGIPSL NALGGVGPV 1080
VPDITIPGIP LSLNALGGVG PIVVPDITIP GIPLSLNALG GVGPIVVPDI TIPGIPSLN 1140
ALGGVGPV PDIPTIPGIP LSLNALGGVG ITVPGVPIR IPLTINIRIP VNITLNEPFP 1200
65 NVAGIFTGYI GPIPLSTFVL GVTLAGGTLE SGIQGFVSN FGLNIPLSGA TNAVITIPGA 1260
INPFGNLVPL SGTSPVTIP GFAINPFGLN VPLSGGTSVP TIPGFTIPGS PLNLTANGGL 1320
GPINIPINIT SAPGFGNSTT TPSSGFFNSG DGSASGFGNV GPGISGLWNQ VPNALQGGVS 1380

GIYNVGQLAS GVANLGNTVS GFNNTSTVGH LTAAFNSGVN NIGQMLLGFF SPGAGP

1436

<212> Type : PRT

<211> Length : 1436

5 SequenceName : SEQ ID 140
SequenceDescription :

Sequence

10 <213> OrganismName : Mycobacterium tuberculosis H37Rv

<400> PreSequenceString :

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	AAAAMAAAAA	PYAGWLGSA	AAAEAVAGQA	RVVVGVEFAA	LAATVDPALV	AANRRLVAL	120
	AVSNLLGQNT	PAIAAAEAAY	ELMWAADVAA	MAGYHSCASA	AAAALPAFSP	PAQALGGGVG	180
15	AFLTALFASP	AKALSLNAGL	GNVGNYNVGL	GNVGVFNLGA	GNVGGQNLGF	GNAGGTNVGF	240
	GNLGNNGVGF	GNSGLGAGLA	GLGNIGLGNA	GSSNYGFANL	GVGNIGFGNT	GTNNVGVGLT	300
	GNHLTGIGGL	NSGTGNIGLF	NSGTGNVGFF	NSGTGNFGVF	NSGNYNTGVG	NAGTASTGLF	360
	NAGNFNTGVV	NVGSYNTGSF	NAGDTNTGGF	NPGGVNTGWL	NTGNTNTGIA	NSGNVNTGAF	420
	ISGNFNNVGL	WVG DYQGLFG	VSAGSSIPAI	PIGLVLNGDI	GPITIQPIPI	LPTIPLSIHQ	480
20	TVNLGLPLVVP	DIVIPAFGGG	IGIPINIGPL	TITPITLFAQ	QTFVNQLPFP	TFSLGKITIP	540
	QIQTTFDSNGQ	LVSFIGPIVI	DTTIPGPTNP	QIDLTIKWDI	PPITLFPNGI	SAPDNPLGLL	600
	VSVSISNPGF	TIPGFSVPAQ	PLPLSIDIEG	QIDGFSTPPI	TIDRIPLTVG	GGVTIGPITI	660
	QGLHIPAAPG	VGN TTTAPSS	GFNSGAGGV	SGFGNVGAGS	SGWWNQAPSA	LLGAGSGVGN	720
	VGTLGSGVLN	LGS GISGFYN	TSVLPFGTPA	AVSGIGNLQ	QLSGVSAAGT	TLRSMLAGNL	780
25	GLANVGNFNT	TFGNGVDVNL	GAANIGGHNL	GLGNVGDGNL	GLGNIGHGNL	GFANLGLTAG	840
	AAGVGNVGF	NAGINNYGLA	NMGVGNIGFA	NTGTGNIGIG	LVGDHRTGIG	GLNSGIGNIG	900
	LFNSGTGNVG	FFNSGTGNFG	IGNSGRFNTG	IGNSGTASTG	LFNAGSFSTG	IANTGDYNTG	960
	SFNAGDTNTG	GFNPGGINTG	WFNTGHANTG	LANAGTFGTG	AFMTGDYSNG	LLWRGGYEGE	1020
	VGVRVGPFTIS	QFPVTVHAIG	GVGPHLVAPV	PVPAVHVEIT	DATVGLGPFT	VPPISIPSLP	1080
30	IASITGSVDL	AANTISPIRA	LDPLAGSIGL	FLEPFRISDP	FITIDAFQV	AGVLFLENII	1140
	VPGLTVSGQI	LVTPTPIPLT	LNLDTTPWTL	FPNGFTIPAQ	TPVTVGMEVA	NDGFTFFPGG	1200
	LTFPRASAGV	TGLSVGLDAF	TLLPDGFTLD	TVPATFDGTI	LIGDIPPIII	DVPAVPGFGN	1260
	TTTAPSSGGF	NTGGGGSGF	ANVGAGTSGW	WNQGHVDLAG	AGSGVANAGT	LSSGVLNVGS	1320
	GISGWYNTST	LGAGTPAVVS	GIGNLGQQLS	GFLANGTVLN	RSPVNIWGA	DVGAFNTGLG	1380
35	NVGDLNWGAA	NIGAQNGLG	NLGSNGVFG	NIGAGNVGFA	NSGPAVLAG	LGNVGLSNAG	1440
	SNNWGLANLG	VGNIGLANTG	TGNIGIGLVG	DYQTGIGGLN	SGSGNIGLFN	SGTGNVGFN	1500
	TGTGNVGLFN	SGSGNIGLGN	SGTGSTGLFN	AGNFNTGIAN	PGSYNTGSFN	VGDTNTGGFN	1560
	PGDINTGWFN	TGIMNTGTRN	TGALMSGTDS	NGMLWRGDHE	GLFGLSYGIT	IPQFPPIRIT	1620
	TGGIGPIVIP	DTTILPPLHL	QTGADADYSF	TVPDIPPIAI	HIGINGVVT	GFTAPEATLL	1680
40	SALKNNGSFI	SFGPITLSNI	DIPPMDFTLG	LPVLGPITGQ	LGPILHLEPI	VAGIGVPLEI	1740
	EPILDAISL	SESPIRIPV	DIPASVIDGI	SMSEVVPIDA	SVDIPAVTIT	GTTISAIPLG	1800
	FDIRTSAGPL	NIPIDIPAA	PGFGNSTQMP	SSGFFNTGAG	GGSGIGNLGA	GVSGLLNQAG	1860
	AGSLVGLTSG	LGNAGTLASG	VLSNGTAISG	LFNVSTLDAT	TPAVISGFSN	LGDHMSGVSI	1920
	DGLIAILTFP	PAESVFDQII	DAAIAELQHL	DIGNALALGN	VGGVNLGLAN	VGEFNLGAGN	1980
45	VGNINVGAGN	LGGNGLGLGN	VGTGNLGFNG	LAGSGVGFNG	AGLTAGAGGL	GNVGLGNAGS	2040
	GSWGLANVGV	GNIGLANTGT	GNIGIGLTGD	YRTGIGGLNS	GTGNLGLFNS	GTGNIGFFNT	2100
	GTGNFGLFNS	GSYSTGVGNA	GTASTGLFNA	GNFNTGLANA	GSYNTGSLNV	GSFNTGGVNP	2160
	GTVNTGWENT	GHTNTGLFNT	GNVNTGAFNS	GSFNNGALWT	GDYHGLVGF	FSIDIAGSTL	2220
	LDLNETNLNG	PIHIEQIDIP	GMSLFDVHEI	VEIGPFTIPQ	VDVPAIPLEI	HESIHMDPV	2280
50	LVPATTIPAQ	TRTIPLDIPA	SPGSTMTLPL	ISMRFEGEDW	ILGSTAAIPN	FGDPFPAPTQ	2340
	GITIHTGPGP	GTTGELKISI	PGFEIPQIAT	TRFLLDVNIS	GGLPAFTLFA	GGLTIPTNAI	2400
	PLTIDASGAL	DPITIFPGGY	TIDPLPLHLA	LNLTVPDSSI	PIIDVPPTPG	FGNTTATPSS	2460
	GFNSGAGGV	SGFGNVGSNL	SGWWNQAASA	LAGSGSVLN	VGTLGSGVLN	VSGSVSGIYN	2520
	TSVLPPLGTPA	VLSGLGNVGH	QLSGVSAAGT	ALNQIPILNI	GLADVGNFNV	GFGNVGDVNL	2580
55	GAANLGAQNL	GLGNVGTGNL	GFANVGHGNI	GFGNSGLTAG	AAGLGNTGFG	NAGSANYGFA	2640
	NQGVNRNIGLA	NTGTGNIGIG	LVGDNLGTIG	GLNSGAGNIG	LFNSGTGNIG	FFNSGTGNFG	2700
	IGNSGSFNTG	IGNSGTGSTG	LFNAGSFNTG	VANAGSYNTG	SFNAGDTNTG	GFNPGTINTG	2760
	WFNTGHTNTG	IANSGNVGTG	AFMSGNFNSG	LLWRGDHEGL	FSLFYSLDVP	RITIVDAHLD	2820
	GGFGPVVLEP	IPVPAVNAHL	TGNVAMGAFT	IPQIDIPALT	PNITGSAAFR	IVVGSVRIPP	2880
60	VSVVIVEQIN	ASVGAEMRID	PFEMWTQGTN	GLGITFYSGF	SADGSPYATG	PLVFGAGTSD	2940
	GSHLTISASS	GAFTTPQLET	GPITLGFQVP	GSVNATILFP	GGLTFPATSL	LNLDTVTAGAG	3000
	GVDIPAITWP	EIAASADGSV	YVLAASSIPLI	NIPPTPGIGN	STITPSSGFF	NAGAGGSGGF	3060
	GNFGAGTSGW	WNQAHTALAG	AGSGFANVGT	LHSGVLNLGS	GVSGIYNTST	LGVGTPALVS	3120
	GLGNVGHQLS	GLLSGGSAVN	PVTVLNIGLA	NVGSHNAGFG	NVGEVNLGAA	NLGAHNLGFG	3180
65	NIGANLGF	NIGHNVGVG	NSGLTAGVPG	LGNAVGLNAG	GNNWGLANVG	VGNIGLANTG	3240
	TGNIGIGLTG	DYQTGIGGLN	SGAGNLGLFN	SGAGNVGFN	TGTGNFGLFN	SGSFNTGVGN	3300
	SGTGSTGLFN	AGSFNTGVAN	AGSYNTGSFN	VGDTNTGGFN	PGSINTGWLN	AGNANTGVAN	3360

	AGNVNTGAFV	TGNFSNGILW	RGDYQGLAGF	AVGYTLPLFP	AVGADVSGGI	GPITVLPPIH	3420
	IPPIPVGFAA	VGGIGPIAIP	DISVPSIHLG	LDPAVHVGS	TVNPITVRTP	PVLVSYSQGA	3480
	VTSTSGPTSE	IWKVPSFFPG	IRIAPSSGGG	ATSTQGAYFV	GPISIPSGTV	TFPGFPTPLD	3540
	PIDIGLPLVSL	TIPGFTIPGG	TLIPTLPLGL	ALSNIGPPVD	IPAIVLDRIL	LDLHADTTIG	3600
5	PINVPIAGFG	GAPGFGNSTT	LPSSGFFNTG	AGGSGGFSNT	GAGMSGLLNA	MSDPLLSAS	3660
	GFANFGTQLS	GILNRGAGIS	GVYNTGALGV	VTAAVVSFGF	NVGQQLSGLL	FTGVGP	3716

<212> Type : PRT

<211> Length : 3716

10 SequenceName : SEQ ID 141
SequenceDescription :

Sequence

15 <213> OrganismName : Mycobacterium tuberculosis H37Rv

<400> PreSequenceString :

	MNFPVLPEPI	NSVLMYSGAG	SSPLLAASAAA	WDGLAEELGS	AAVSFGQVTS	GLTAGVWQGA	60
	AAAAAASAAA	PYAGWLGSVA	AQAVAVAGQA	RAAVAAFEAA	LAATVDPAAV	AVNRMAMRAL	120
	AMSNLLGQNA	AAIAAVEAEY	ELMWAADVAA	MAGYHSGASA	AAAALPAFSP	PAQALGGGVG	180
20	AFLNALFAGP	AKMLRLNAGL	GNVGNYNVGL	GNVGIFNLGA	ANVGAQNLGA	ANAGSGNFGF	240
	GNIGNANFGF	GNSGLGLPPG	MGNIGLGNAG	SSNYGLANLG	VGNIGFANTG	SNNIGIGLGT	300
	DNLTGIGGLN	SGTGNLGLFN	SGTGNIGFFN	SGTGNFGVFN	SGSYNTGVGN	AGTASTGLFN	360
	VGGFNTGVAN	VGSYNTGSFN	AGNTNTGGFN	PGNVNTGWLN	TGNTNTGIAN	SGNVNTGAFI	420
	SGNFSNGVLW	RGDYEGLWGL	SGGSTIPAIP	IGLELNGGVG	PITVLPPIQL	PTIPLNIHOT	480
25	FSLGLPLVVD	IVIPAFGGGT	AIPISVGPIT	ISPTLFPAP	NFNTTFPVGP	FFGLGVVNIS	540
	GIEIKDLAGN	VTLQLGNLNI	DTRINQSFV	TVNWSTPAVT	IFPNGISIPN	NPLALLASAS	600
	IGTLGFTIPG	FTIPAAPLPL	TIDIDGQIDG	FSTPPTITDR	IPNLNGASVT	VGPILINGVN	660
	IPATPGFGNT	TTAPSSGGFN	SGDGGVSGFG	NFGAGSSGWW	NQAQTEVAGA	GSGFANFGSL	720
	GSGVLNFGSG	GSGLYNTGGL	PPGTPAVVSG	IGNVGEQLSG	LSSAGTALNQ	SLIINLGLAD	780
30	VGSVNVGFGN	VGDFNLGAAN	IGDLNVGLGN	VGGGNVGFEN	IGDANFGLGN	AGLAAGLAGV	840
	GNIGLGNAGS	GNVGFNGMGV	GNIGFGNTGT	NNLGLGLTGD	NQTGIGGLNS	GAGNIGLFNS	900
	GTGNVGLFNS	GTGNFGLFNS	GSFNTGIGNG	GTGSTGLFNA	GNFNTGVANP	GSYNTGSFNV	960
	GDNTGIDVPA	IVIPAFGGGT	GNANTGVANS	GNVDTGALMS	GNFNGILWR	GNFEGFLGLN	1020
	VGITIEPFPI	HWTSTGGIGP	IIIPDITILP	PIHLGLTGQA	NYGFAVPDIP	IPAIHIDFDG	1080
35	AADAGFTAPA	TTLLSALGIT	GQFRFGPITV	SNVQLNPFNV	NLKLQFLHDA	FPNEFPDPTI	1140
	SVQIQVAIPL	TSATLGLLAL	PLQQTIDAIE	LPAISFSQSI	PIDIPPIDIP	ASTINGISMS	1200
	EVVPIDVSPD	IPAVTITGTR	IDPIPLNFDV	GNSTELPSSG	GNSTELPSSG	GNSTELPSSG	1260
	FFNTGGGGGS	GIANFGAGVS	GLLNQASSPM	VGTLSGLGNA	GSLASGVVNS	GVDISGMFNV	1320
	STLGSAPAVI	SGFGNLGNHV	SGVSIIDGLA	MLTSGSGSGS	GQPSIIDAAI	AELRHLNPLN	1380
40	IVNLGNVGSY	NLGFANVGDV	NLGAAGNLGN	NLGGGNLGGQ	NLGLGNLGDG	NVGFNGLGHG	1440
	NVFGNLSGLG	ALPGIGNIGL	GNAGSNNVGF	GNMGLGNIGF	GNVTGNLNLGI	GLTGDNQTGF	1500
	GGLNSGAGNL	GLFNSGTGNI	GGFNTGTGNW	GLFNSGSYNT	GIGNSGTGST	GLFNAGSFNT	1560
	GLANAGSYNT	GSLNAGNTNT	GGFNPNGVNT	GWFNAGHTNT	GGFNTGNVNT	GAFNSGSFNN	1620
	GALWTGDHGH	LVGFYSYSIE	TGSTLVVDINE	TLNLGPVHID	QIDIPGMSLF	DIHELNVNIGP	1680
45	FRIEPIDVPA	LVDIHEHMTV	IPPIVFLPSM	TIGGQTYTIP	LDTPPAPAPP	PFRLPLLFVN	1740
	ALGDNWIVGA	SNSTGMSGGF	VTAPTQIGILI	HTGPSSATTG	SLALTLPTVT	IPTITTSPIP	1800
	LKIDVSGGLP	AFTLFPGLLN	IPQNAIPLTI	DASGVLDPIIT	IFPGGFTIDP	LPLSLALNIS	1860
	VPDSSVPIII	VPPTPGFGNA	TATPSSGGFN	SGAGGVSGFG	NFGAGSSGWW	NQAHAALAGA	1920
	GSGVLNVGTL	NSGVNLVSGS	ISGLYNTAIV	GLGTPALVSG	AGNVGQQLSG	VLAAGTALTQ	1980
50	SPIINLGLAD	VGNYNLGLGN	VGDFNLGAAN	LGDLNLGLGN	IGNANVGFEN	IGHGNVGFEN	2040
	SGLGAALGIG	NIGLGNAGST	NVGLANMGVG	NIGFANTGTN	NLGLGLTGDN	QTGIGGLNSG	2100
	AGNIGLFNSG	TGNIGFFNSG	TGNWGLFNNG	SFNTGIGNSG	TGSTGLFNAG	GFTTGLANAG	2160
	SYNTGSENVG	DTNTGGFNPG	SINTGWFTNG	NANTGIANSG	NVDTGALMSG	NFSNGILWRG	2220
	NYEGLFSYSY	SLDVPRITIL	DAHFTGAFGP	VVVPPIPVLA	INAHLTGNAA	MGAFTIPQID	2280
55	IPALNPVNTG	SVGFGPPIAVP	SVTIPALTAA	RAVLDMASV	GATSEIEPFI	VWTSSGAIGP	2340
	TWYSVGRIYN	AGDLFVGGN	ISGIPTLSTT	GPVHAVFNAA	SQAFNTPALN	IHQIPLGFQV	2400
	PGSIDAITLF	PVGLTFPANS	LLNLDVFGVT	PGATIPAITF	PEIPANADGE	LYVIAGDIPL	2460
	INIPPTPGIG	NTTVPSSSGF	FNTGAGGGSG	FGNFGANMSG	WWNQAHTALA	GAGSGIANVG	2520
	TLHSGVLNLG	SGLSGIYNTS	TLPLGTALV	SGLGNVGDHL	SGLLASNVGQ	NPITIVNIGL	2580
60	ANVGNGNVGL	GNIGNLNLGA	ANIGDVNLGF	GNIGDVNLGF	GNIGGGNVGF	GNIGDANFGF	2640
	GNSGLAAGLA	GNIGNLNLGA	GNIGNLNLGA	GNIGNLNLGA	GNIGNLNLGA	GNIGNLNLGA	2700
	NSGTGNIGLF	NSGTGNIGFF	NSGTANFGLF	NSGSYNTGIG	NSGVASTGLV	NAGGFNTGVA	2760
	NAGSYNTGSF	NAGDTNTGGF	NPGSTNTGWF	NTGNANTGVA	NAGNVNTGAL	ITGNFSNGIL	2820
	WRGNYEGLAG	FSFGYPIPLF	PAVGADVTDG	IGPATIIPPI	HIPSIPLGFA	AIGHIGPISI	2880
65	PNIAIPSIHL	GIDPTFDVGP	ITVDPITLTI	GLSLDAAVS	EIRMTSGSSS	GFKVRPSFSF	2940
	FAVGPDGMPG	GEVSILQPFT	VAPINLNPTT	LHFPGFTIPT	GPIHIGLPLS	LTIPGFTIPG	3000
	GTLIPQLPLG	LGLSGGTPPF	DLPTVVIDRI	PVELHASTTI	GPVSLPIFGF	GGAPGFGNDT	3060

TAPSSGFFNT GGGGSGFSN SGSGMSGVLN AISDPLLGS A SGFANFGTQL SGILNRGAGI 3120
SGVYNTGTLG LVTSAFVSGF MNVQQQLSGL LFAGTGP 3157

<212> Type : PRT

<211> Length : 3157

5 SequenceName : SEQ ID 142
SequenceDescription :

Sequence

10 <213> OrganismName : Mycobacterium tuberculosis H37Rv

<400> PreSequenceString :

MSFVVMPEEI NSLLIYTGAG PGPILLAAAA WDELAELGS AAAAFGSVTS GLVGGIWQGP 60
SSVAMAAAA PYAGWLSAAA ASAESAGQA RAVVGVFEEA LAETVDPFVI AANRSRLVSL 120
ALSNLFGQNT PAIAAAEFDY ELMWAQDVAA MLGYHTGASA AAEALAPFGS PLASLAAAAE 180
15 PAKSLAVNLG LANVGLFNAG SGNVGSYNVG AGNVGSYNVG GGNIGGNNVG LGNVGWGNFG 240
LGNSGLTPGL MGLGNIGFGN AGSYNFGLAN MGVGNIGFAN TGSGNFGIGL TGDNLGTGFG 300
FNTGSGNVGL FNSGTGNVGF FNSGTGNWGV FNSGSYNTGI GNSGIASLGL FNAGGFNTGV 360
VNAGSYNTGS FNAGEANTGG FNPGSVNTGW LNTGDINTGV ANSGDVNTGA FISGNYSNGV 420
LWRGDYQGLL GFSSGANVLP VIPLSLDING GVGAITIEPI HILPDIPINI NETLYLGPLV 480
20 VPPINVP AIS LGVGIPNISI GPIKINPITL WPAQNFNQTI TLAWPVSSIT IPQIQQVALS 540
PSPIPTTLIG PIHINTGFSI PVTFSYSTPA LTLFPVGLSI PTGGPLTLTL GTTAGTEAFT 600
IPGFSIPEQP LPLAINVIGH INALSTPAIT IDNIPLNLHA IGGVGPVDIV GGNVPASPGF 660
GNSTTAPSSG FFNTGAGGVS GFENVGAAHTS GWFNQSTQAM QVLPGTVSGY FNSGTLMSGI 720
GNVGTQLSGM LSGGALGGNN FGLGNIGFDN VGFGNAGSSN FGLANMGIGN IGLANTGNNG 780
25 IGI LSGDNL TGFGGFNSGS ENVLGNISGT GNVGSYNTGI GNLGVFNSSG HNTGFFLTGN 840
NINVLAPFTP GTLFTISEIP IDLQVIGGIG PIHVQPIDIP AFDIQTGGF IGIREFTLPE 900
ITIPAIPHV TGTVGLGEGF VNPAPVLFQ TAMAETADP VVLPDPFITI DHYGPPLGPP 960
GAKFPSSGFY LSISDLQING PIIGSYGGPG TIPGPFPGATF NLSTSSIALF PAGLTVPDQT 1020
PVTVNLTGGL DSITLFPGL AFPENPVVSL TNFSVGTGGF TVFPQGTVD RIPVDLHTTL 1080
30 SIGPFPFRWD YIPPTPANG IPAVPGGFL TSGLFPFHFT LGGGIGPISI PTTTVVDALN 1140
PLLTVTGNLE VGPFTVPDIP IPAINFGLDG NVNVSFNAPA TTLGLGLGIT GSIDISGIQI 1200
TNIQTQPAQL FMSVGQTLFL FDFRDGIELN PIVIPGSSIP ITMAGLSIPL PTVSESIPLN 1260
PSFGSPASTV KSMILHEILP IDVSINLEDA VFIPATVLP IPLNVDTVIP VGPINIPIT 1320
EPGSGNSTTT TSDPFSGLAV PGLGVGLLGL FDGSIANNLI SGFNSAVGIV GPNVGLSNLG 1380
35 GGNVGLGNVG DFNLGAGNVG GFNVGGGNIG GNVVGLGNVG FGNVGLANS LTPGLMGLGN 1440
IGFGNAGSYN FGLANMGVGN IGFA NTGSGN FGIGLTGDNL TGFGGFNTGS GNVGLFNSTG 1500
GNVGFNTSGT GLGNVGVGNF GLGNISLTPG LMGLGNIGF NAGSYNFGLA NMGVGNIGFA 1560
ANTGGFNP GS VNTGWLNTGD INTGVANS GD VNTGAFISGN YSNGAFWRGD YQGLLGFSYR 1620
PAVLPQT PFL DLTLTGGLGS VVIPAIDIPA IRPEFSANVA IDSFTVPSIP IPQIDLAATT 1680
40 VSVGLGPITV PHLDIPRPV TNLVLFSGSQ GGPLKIGPIT GLFNTPIGLT PLALSQIVIG 1740
ASSSQGTITA FLANLPFSTP VVTIDEIPLL ASITGHSEPV DIFPGGLTIP AMNPLSINLS 1800
GGTGAVTIPA ITIGEIPFDL VAHSTLGPVH ILIDLPAVPG FGNTTGAPSS GFFNSGAGGV 1860
SGFGNVGAMV SGGWNQAPSA LLGGSGGVFN AGTLHSGVLN FGSGMSGFLN TSVLGLGAPA 1920
LVSGLSVGQ QLSGLLASGT ALHQGLVLNF GLADVGLGNV GLGNVGDFNL GAGNVGGFNV 1980
45 GGNIGGNV GLGNVGVGNF GLGNISLTPG LMGLGNIGF NAGSYNFGLA NMGVGNIGFA 2040
NTGSGNFGIG LTGDNLTGFG GFNTGSGNVG LFNSGTGNVG FFNSGTGNWG VFNSGSYNTG 2100
IGNSGIASTG LFNAGGFNTG VVNAGSYNTG SFNAGQANTG GFNPGSVNTG WLNTGDINTG 2160
VANSGDVNTG AFISGNYSNG AFWRGDYQGL LGFSYTSITII PEFTVANIHA SGGAGPIIVP 2220
SIQFPAIPLD LSATGHIGGF TIPPVSISPI TVRIDPVFDL GPITVQDITI PALGLDPATG 2280
50 VTVGPIFSSG SIIDPFSLTL LGFINVNVA IQTAPSEILP FTVLLSSLGV THLTPEITIP 2340
GFHIPVDPIH VELPLSVTIG PFVSPFITIP QLPLGLALSG ATPAFAPLE ITIDRIPVVL 2400
DVNALLGPIN AGLVIPPVPG FGNTTAVPSS GFFNIGGGGG LSGFHNLAG MSGVLNAISD 2460
PLLSASGFA NFGTQLSGIL NRGADISGVY NTGALGLITS ALVSGFGNVG QQLAGLIYTG 2520
TGP 2523

55 <212> Type : PRT

<211> Length : 2523

SequenceName : SEQ ID 143
SequenceDescription :

Sequence

60 <213> OrganismName : Mycobacterium tuberculosis H37Rv

<400> PreSequenceString :

MSFVIAVPEA LTMAASDLAN IGSTINAANA AAALPTTGTV AAADEVSA VAALFGSYAQ 60
65 SYQAFGAQLS AFHAQFVQSL TNGARSYVVA EATSAAPLQD LLGVVNAPAQ ALLGRPLIGN 120
GANGADGTGA PGGPGGLLLG NNGNGSGCAP GQPGGAGGDA GLIGNGGTGG KGGDGLVGSG 180
AAGGVGGRGG WLLNGGTGG AGGAAGATLV GGTGGVGGAT GLIGSGGFGG AGGAAAGVGT 240

TGGVGGSGGV GGVFGNGGFG GAGGLGAAGG VGGAAASYFGT GGGGGVGGDG APGGDGGAGP 300
LLTGNGGVVG LGGAGAAAGN GGAGGMLLD GGAGGQGGPA VAGVLGMPG AGGNGGNANW 360
FGSGGAGGQG GTGLAGTNGV NPGSIANPNT GANGTDNSGN GNQTGGNGGP GPAGGVGEAG 420
GVGGQGGGLGE SLGDNDGTGG KGGAGGTAGT DGGAGGAGGA GGIGETDGS A GGVATGGEGG 480
5 DGATGGVDGG VGGAGGKGGQ GHNTGVGDAF GGDGGIGGDG NGALGAAGN GGTGGAGNG 540
GRGMLIGNG GAGGAGGTGG TGGGGAAGFA GGVGGAGGEG LTDGAGTAEG GTGGLGGLGG 600
VGGTGGMGGG GGVGGNGGAA GSLIGLGGGG GAGGVGGTGG IGGIGGAGN GGAGGATTT 660
GGGATIGGGG GTGGVGGAGG TGGTGGAGGT TGGSGGAGL IGWAGAAGGT GAGGTGGQGG 720
LGGQGGNGN GGTGATGGQG GDFALGGNGG AGGAGGSPGG SSGIQNMGP PGTQGADG 778

10 <212> Type : PRT
<211> Length : 778
SequenceName : SEQ ID 144
SequenceDescription :

15 Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

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QQNGNGNGGN GGTGGKGGTG GDGALAGSSG GAGGKGGNGG DAGKAGTGS A PCTAGTGGDG 120
GKGGNGGIGA AGTTGPVGTG ASGGTGGSGG AGGTGGDGGA ANGGTAGAGG AGGNGKGGD 180
GGAGVTSSTA GNSGGAGGSG GKGGDAGAGG AGATPGANGI AGNGGDGGDG AAGAVGISGA 240
TGAGDGGHGG TGAAGGNGGT GGAGGSGIDG VGGGTGGTGG NGNGAIGGA GGDAGGSGNS 300
25 GNGGGIGGKG GNAGAGGAAG SNGGTVGANG TGGDGGNGGA AGAATAGSNG GAGTGSAGNG 360
GGTGGRGSSG GAGGDGIGGV GGGKGGNGAD GEVGGAGGAG GSGPNTSPGG NGGQGGQGGG 420
GGAGGAAGAG GAGGGANGTA GNGGQGGAGG TGGAGAASSA TNGGSGGAGG TGGDGGSGGA 480
GGTGGAGGTG GAAGDGGQGG QGGAGGGAGG QGGAGGAGGT GNGNGNITGG TAGTAGAAGN 540
GGAAGKGGAG QGGTGGGTG QGGAGGDDG AGGTGGDRTV GGGTVPAGSG GQGGNAGGGG 600
30 AGGQGGADGG SGGDGGDAGT GNGNGNGNR NSGNGTGGAG GNGGGGANGG AGGAGGSGGG 660
TGGNGGAGGD AGDAGNGNG NGTGNGNGG NGGIAGMGGN GGAGTGSNG GNGSGGNGG 720
NAGMGGNSGT GSGDGGAGGN GGAAGTGGTG GDGGLTGTGG TGGSGGTGGD GNGGNGADN 780
TANMTAQAGG DGGNGDGGF GGGAGAGGGG LTAGANGTGG QGGAGDGGN GAI GGHGPLT 840
DDPGGNGGTG GNGGTGGTGG AGIGSLGGT GGDGGNGNG GTGEGGGEVG GAGGTGGAAG 900
35 NGGDGGTGGT GGGDGGAGGT GGTGGTGGLG DPRVGGSGGD GGTGGSGGAA GNGGNGNAG 960
AGGNGNGGTG GAGGIGGTGG NGGDAEPGVP PGAGGAGGAG TTGGKGGTGG NGS GTSGGT 1020
GGDGGTGGGG GNGGTGWNNG KGD TGS GGA GDGKAPAGG TGGAGDGGA GKGSGGV 1079

40 <212> Type : PRT
<211> Length : 1079
SequenceName : SEQ ID 145
SequenceDescription :

45 Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

50 MVMSLMVAPE LVAAAAADLT GIGQAISAN AAAAGPTTQV LAAAGDEVSA AIAALFGTHA 60
QEYQALSARV ATFHEQFVRS LTAAGSAYAT AEAANASPLQ ALEQQVLGAI NAPTQLWLGR 120
PLIGDGVHGA PGTGQPGGAG GLLWNGGNG GSGAAGQVGG PGGAAGLFGN GSGSGSGGAG 180
AAGGVGGSGG WLNNGGAGG AGGTGANGGA GGNAWLFGAG GSGGAGTNGG VGGSGGFVYG 240
NGGAGGIGGI GGIGNGGDA GLFNGGAGG AGAAGLPAA GLNGGDGSDG GNGGTGGNGG 300
RGGLLVNGG AGGAGGVGGD GKGGAGDPS FAVNNGAGN GGHGNGPVG GAGGAGLLA 360
GAHGAAGATP TSGGNGDGG IGATANSPLQ AGGAGGNGGH GGLVNGGTG GAGGAGHAGS 420
55 TGATGTALQP TGGNGTNGGA GGHGNGGNG GAQHGDGGVG GKGGAGSGG AGGNGFDAAT 480
LGSPGADGGM GNGGKGGDG GKAGDGGAGA AGDVTLAVNQ GAGGDGGNGG EVGVGGKGA 540
GGVSANPALN GSAGANGTAP TSGGNGNGG AGATPTVAGE NGGAGGNGGH GGSVNGGAG 600
GAGGNGVAGT GLALNGGNG NGGIGNGGS AAGTGGDGGK GNGGAGANG QDFSASANGA 660
NGGQCGNGGN GGIGGKGGDA FATFAKAGN GAGGNGGNGV VAGQGGAGGK GAI PAMKAT 720
60 GADGTAPTSG GDGNGNGGA SPTVAGNGG DGGKGGSGN VNGGNGGAG GNGAAGQAGT 780
PGFTSGDSTG SGTGGAGGN GGAGGAGTL AGHGGNGKG GNGGQGGIGG AGERGADGAG 840
PNANGANGEN GSGGNGGDG GAGGNGGAGG KAQAAGYTDG ATGTGGDGGN GGDGGKAGD 900
GAGENGLNSG AMLPGGTVG NPGTGGNGN GGNAGVGGT GKAGTGSITG LDGTDGITPN 960
GNGGNGGNG GKGGTAGNS GAAGNGGNG GGLNGGDAG NGGNGGALN QAGFFGTGGK 1020
65 GNGGNGGAG MINGGLGGF GAGGGGAVDV AATTGGAGN GGAGGFASTG LGGPGGAGG 1080
GGAGDFASGV GGVGGAGGD GAGGVGGFGG QGIGGEGRT GNGGSGGDG GGGISLGGN 1140
GLGGNGGVSE TGFGGAGNG GYGGPGGPEG NGGLGGNGA GNGGVSTTG GDGAGGKGG 1200

5 NGGDGGNVGL GGDAGSGGAG GNGGIGTDAG GAGGAGGAGG NGGSSKSTTT GNAGSGGAGG 1260
NGGTGLNGAG GAGGAGGNAG VAGVSFGNAV GGDGNGGNG GHGGDGTGG AGGKGGNGSS 1320
GAASGSGVNV VTAGHGGNGG NGNGGGNGSA GAGGQGGAGG SAGNGGHGGG ATGGDGGNGG 1380
NGGNSGNSTG VAGLAGGAAG AGGNGGGTSS AAGHGGSGGS GSGTGTGGAG AAGGNGGAGA 1440
GGGSLSTGQS GGP RRQRWCR WQRRRWLGRQ RRRRWCRWQR RCRRQRWRR CRQRRLRRQW 1500
RQRRRRCRPW LHRRRRGRQGR RWRQRRFQQR QRSRWQRR 1538
<212> Type : PRT
<211> Length : 1538
SequenceName : SEQ ID 146
SequenceDescription :

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Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVV TAPPV LASAASDLGG IASMISEANA MAAVRTTALA PAAADEVSAA IAALFSSYAR 60
DYQTL SVQVT AFHVQFAQTL TNAGQLYAVV DVGNVLLKT EQQVLGVINA PTQTLVGRPL 120
IGDGT H GAPG TGQNGGAGGI LWGNGGNGGS GAPGQPGGRG GDAGLFGHGG HGGVGGPGIA 180
GAAGTAGLPG GNGANGSGSG IGGAGGAGGN GGLLFGNGGA GGQGGSGGLG GSGGTGGAGM 240
AAGPAGGTGG IGGIGGIGGA GGVGGHGSAL FGHGGINGDG GTGGMGGQGG AGNGWAAEG 300
ITVIGIEQGG QGGDGGAGGA GGIGGSAGGI GGSQAGGHG GDGGQGGAGG SGVGGGGAG 360
AGDGGAGGI GGTGNGSIG GAAGNGNGG RGGAGGMATA GSDGNGGGG GNGGVGVGSA 420
GGAGGTGGDG GAAGAGGAPG HGYPQQPAPQ GLPIGTGGTG GEGGAGGAGG DGGQGDIGFD 480
GGRGGDGGPG GGGGAGGDGS GTFNAQANNG GDGGAGGVGG AGGTGGTGGV GADGGRGGDS 540
GRGGDGGNAG HGGAAQFSGR GAYGEGGSG GAGGNAGGAG TGGTAGSGGA GFGGNGADG 600
GNGGNGGNGG FGGINGTFGT NGAGGTGGLG TLLGHNNGNI GLNGATGGIG STTLTNATVP 660
LQLVNTTEPV VFISLNGGQM VPVLLDTGST GLVMSQFLT QNFGPVI GTG TAGYAGGLTY 720
NYNTYSTTVD FGNGLLTLEPT SVNVTSSSP GTLGNFLSRS GAVGVLGIGP NNGFPGTSSI 780
VTAMPGLLNN GVLIDESAGI LQFGPNTLTG GITISGAPIS TVAVQIDNGP LQQAPVMFDS 840
GGINGTIPSA LASLPSGGFV PAGTTISVYT SDGQTL LYSY TTTATNTPFV TSGGVMNTGH 900
VPFAQQPIYV SYSPTAIGTT TFN 923
<212> Type : PRT
<211> Length : 923
SequenceName : SEQ ID 147
SequenceDescription :

35
Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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GAGGAGGSGG SGAAGCAGGA GGAGGLFASG GSGGFGGFAS TGTGGAGGTG GAGGLFASGG 120
VGGTGGGAGS GGTGGVGGTG GAGGLFASGG AGGAGGSGGT GGAGGTGGAG GLFGAGGAGG 180
LGGQGNHTGG HGGAGGSAGL LALGDGAGG AGGAATTGTG GAGGAGGKAG LLFGSGGAGG 240
SGGAAGTFGD TGNSGGAGGA GKAGLLFGS GGAGGSGGAG GFANGSTGGA GGAGGGAGLI 300
GNGGNGGSGG TSVATGGAGN GGAGGAGGGA GLIGNGNGG SSGMGDAPGG TGVGGIGGLL 360
LGLDGANAPA STNPLHTAQQ QALAAVNAPI QAVTGRPLIG NGANGAPGSG APGGHGGWLF 420
GGGGTGGSGV SGGAGGDGGA GGILFGAGGA GGAGGAVTGT GATGSGGGAG GALLFGAGG 480
AGGAGGSSGI GGFAAGGAGG PGAGGLFNG GGAGGAGSG VSGGAGGEGG AGGAGGLFAG 540
GGAGGAGGSG NNVGAGGAG GVGGLFGAGG AGGSGGGSV AGDSGAGGNA GLLAPGLAGG 600
AGGGGGQGF D TGGAGGPGD AGLLVGSGGV GGAGGFGLTT GGPAAAGGDA GLLFGSGGAG 660
GAGGSGRTDL GGAGGAGGKA GLIGNGNGG AGGAGGNGG DGGPGGAAGF LGNGGNGGNG 720
GTGTSAGSPG AGGAGGSLIG AEGLPGLLP 749
<212> Type : PRT
<211> Length : 749
SequenceName : SEQ ID 148
SequenceDescription :

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Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVIAAPEA LVAVASDLAG IGSALAEANA AALAPTTALL AAGADEVSAA IAALFGAHGQ 60
AYQTVSAQAS AFHAQFVQAL TGGGGAYAAA EAA NVSAAQS TDQRLLDLIN GPTQALLGRP 120
LIGDGANGGP QDGGPGGLL YGNGGNGGTS TTAGVAGGNG GAAGLIGNGG AGGGGGAGAA 180
GGNGGAGGWL YGNGGAGGAG GTSVIPGVAG NNGGAGGSAG LWGTGGAGG GNGRSGPVN 240
VAGSAGGNGG AGGAAGLFGD AGAGGNGGKG GAGGAASF SIN FTAGDGGAGG AGSGGHHALL 300

WGAGGAGGNG GSGGTGGAGG STAGAGGNGG AGGGGGTGGL LFGNGGAGGH GAAAGNGLAA 360
GNGVSSSSGG GAGGTGGAGG DGGAGGAGGN ARLWGVGGAG GAGGDGGAGG AGGKGGSGLS 420
GNANGGAGGD SGRGGTGGAG GEGGAAGLLV GTGGHGGDGG AGGAAVKGGD GGAAAGTGIA 480
GAGGRGGAGG SGGSGGDGGG GAAGPAGWLF GDGGAGGNGG AAAAGGAGGQ AGGGGGNNGN 540
5 GNGGNGGNG GNGATGGWLY GNGGAGGQCA TAGAGGAGAN GVSSTNGGGT GNGGGIGGTG 600
GSGGAGGNAG LLGVGGAGGH GASGGACDRG GAGGTGFISS DGGAGGDGGD GNGGAGGTG 660
GLLFAGGNG GPGGSGGAAD ICGNGGAGNG GGTDCNGNGG GSGGGAGSGG DGGGAGGNGA 720
WLFNGGAGG GGGKGGNGAG GGLGGGSFGL PGLNGSGGDG GDGGNGAPGG VLYGNGGAGG 780
QSSSGGIGGP GATGGAGGKG GDGGDAQLIG DGGNGNGGA GGTGGTPGPG GPGGSGGLGG 840
10 LLFGQTGTAG VSP 853
<212> Type : PRT
<211> Length : 853
SequenceName : SEQ ID 149
SequenceDescription :
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<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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AYQALSAQAA MFHEQFVRAL AAGGNSYAVA EAATAQSVQQ DLLNLINAPT QALLGRPLIG 120
NGANGLPGTG QNGGDGGILY GNGGNGSGG VNQAGGNGN AGLWNGGSG GAGGNATTAG 180
RNGFNAGGAG SGGLLWNGG AGGAGGNGGP APLVGGVGTG GAGGNGGGA GLFYGFGGAG 240
GNGMGGVAP STGPSMILP AGGVGGPGGS GGASALAFGS GGVGGAGGLG GPTDGTVQGV 300
25 GGFPGGGNG IGGLLFGNA GAGGAGAAG AGTGDTEFSG GHGGAGDGG AVGLIGNGGA 360
GGTGSPPGAV GNGGVGGGLG GAGSPGGLLY GTGGAGGNG PGDDGGTGAT VGFAGSGGFG 420
GAGGIAQLFG TGGMGGSGG IGAGTTTVVP PDVAPVGGTG GNGGRAGLLL GVGMGGNGG 480
ATSVGGTLYA AGNGGDGGL VWGNGGTGGS GGAGGAGSVG NGGAGGNAAL LFGNGGAGGA 540
GGAGGIGAGG AGGFGAVLFG NGGAGGSGAP GGIGAGGNG NALLVNGGN GGAGTGAAG 600
30 GAGGSGGLLF GQNGMPGP 618
<212> Type : PRT
<211> Length : 618
SequenceName : SEQ ID 150
SequenceDescription :
35
Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
40 MNFSLPPEI NSALIFAGAG PEPMAAATA WDGLAMELAS AAASFSGSVTS GLVGGAWQGA 60
SSSMAAAAA PYAAWLAAA VQAEQTAQA AAMIAEFEAV KTAVVQPM LV AANRADLVSL 120
VMSNLFGQNA PAIAAIEATY EQMWAADVSA MSAYHAGASA IASALSPFSK PLQNLAGLPA 180
WLASGAPAAA MTAAAGIPAL AGGPTAINLG IANVGGGNGV NANNGLANIG NANLGNYNFG 240
SGNFNGSNIG SASLGNNGN FGNLGSNNVG VGNLGNLNTG FANTGLGNFG FGNTGNMNG 300
45 IGLTGNNGIG IGGLNSGTGN FGLFNSGSGN VGFFNSGNGN FGIGNSGNEN TGGWNSGHGN 360
TGFFNAGSFN TGMLDVGNAN TGSNTGSGN MGDFNPGSSN TGTFNTGNAN TGFLNAGNIN 420
TGVFNIGHMN NGLFNTGDMN NGVFYRGVQ GSLQFSITTP DLTLPPLQIP GISVPAFSLP 480
AITLPSLNIP AATTPANITV GAFSLPGLTL PSLNIPAAAT PANITVGAFS LPGLTLPSLN 540
IPAATTPANI TVGAFSLPGL TLPNIPAA TTPANITVGA FSLPGLTLPS LNIPAAATPA 600
50 NITVGAFSLP GLTLPSLNIP AATTPANITV SGFQLPPLSI PSVAIPPVTV PPITVGAFNL 660
PPLQIPEVTI PQLTIPAGIT IGGFSLPAIH TQPIITVGQIG VQFGLPSIG WDVFLSTPRI 720
TVPAFGIPFT LQFQTNVPAL QPPGGGLSTF TNGALIFGEF DLPQLVHPY TLTGPIVIGS 780
FFLPAFNIPG IDVPAINVDG FTLPQITTPA ITTPEFAIPP IGVGFTLPQ ITTQEIITPE 840
LTINSIGVGG FTLPQITTP ITTPTITIDP INLTGFTLPQ ITTPTITTP LTIDPINLTG 900
55 FTLPQITTP ITTPTITIEP IGVGFTTP LTVPGIHLPS TTIGAFAPG GPGYFNSSTA 960
PSSGFFNSGA GNSGFGNGG SGLSGWFNTN PAGLLGSGY QNFGGLSSGF SNLGSVSGF 1020
ANRGILPFSV ASVVS GFANI GTNLGFFQG TTS 1053
<212> Type : PRT
<211> Length : 1053
SequenceName : SEQ ID 151
SequenceDescription :
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<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
65 MLYVVASPD LMTAAATNLAE IGSAISTANG AAALPTVEVV AAADEVSTQ IAAALFGAHR 60

SYQTLSTQAA AFHSRFVQAL TTAAASYASV EAANASPLQV ALDVINAPAQ TLLGRPLIGN 120
GADGSTPGQA GPGGGLLYGN GGNGAAGGPN QAGGAGGNAG LIGNGGAGGA GGVGAVGGKR 180
GTGGLLFGNG GAGGQGGGLG AGINGGSGGQ GGHGGNAILF GQGGAGGPGG TGAMGVAGTN 240
PTPIGTAAFG SDGVNQIGNG GNTDLTGGAG GDNAGSTTV NGNGGTGGA ARNSSGGTGN 300
5 SFGGAGGAGG DGANGGDGGA GGEALTEGGA TAVSGAGGKG GNAEASGGAG GNGGKGGFAQ 360
ATTSVTGGNG GNGGNHDSN APGGAGGSGG VGGDGGRGGL LAGNGGTGGA GNGGTGGAG 420
APGGAGGAGG KADIANSLGD NATVTGGNGG TGGDGGGSGG TGGAGGAGGL GGHGAGGGLL 480
ICNGGAGGAG GLGGAGGAGG AGGEGGAGGA GGEAIPGGAS TNSAGGDGGA GGTGCGGGDG 540
GAGGAPGLGG AGGAGGWLIG QSGSTGGGGA GGAGGAGGAG GAGGSGGAGG HGDTSKGNG 600
10 SSGTAGFDGN PGQPG 615
<212> Type : PRT
<211> Length : 615
SequenceName : SEQ ID 152
SequenceDescription :
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Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
20 MHYSVLPEI NSALIFAGAG SGPMLAAASA WDGLATELAS AAVSFGSVTA GLVGGSWQGR 60
SSVMAAAAA PYAGWLAAAA TQAEQAATQA QVMVAEFEAV RLAMVQPALV AANRSGLISL 120
VISNLFQNA PAIAAAEAAY EEMWALDVSA MAAYHSGASA VAVALPAFAL PLRLPAGLAA 180
GPAAVVTALT TAVGMPTFAG RAIAASLGLA NVGGGNLGNNA NNGLGNIGNA NLGNNNLGSG 240
NFGSFNIGSA NLGNNNIGIG NAGANNFGLA NLGNLNTGFA NAGIGNFGIA NTGNNNIGNG 300
25 LTGNNQIGIG GLNSGNGNVG LFNAGSANIG FPNSGNGNFG IGNSGNFSTG LFNPGHGNTG 360
FLNAGSFNTG MFDVGNANTG SFNVGHYNGF AFNPGPSNTG TFNTGGANTG WFNTGSINTG 420
AFNIGDMNNG LFNTGDMNNG VFYRGVQGS LQFAITSPDL TLPSLEIPGI SVPAFSLPAI 480
TLPSLTIPAV TTPANVTGA FDLPLGLTVPS LTTPAAMTPA NITVGAFDLP GLTVPSLTIP 540
ATTPANITV GAFNLQQLSI PSVTVPPI TI PAGTALGAFN LPTLSIPSVT VPPITIPAGT 600
30 TVGGFTLPTI HTPLISTPQI SIGGFSTPGI ATQANSQVIN LPTFSLNGIT ITNLVVFIPN 660
NTALQTNMP GVFPQIGGFA NTPPAFINTG TITVGGGQIN GVGFSIGAIN VTPFTLENVV 720
IQPWSLGGIS VDGFTLPEIS TQEFFTPALT ISPIGVGALS LPDITTTQFT TPELTIDPIT 780
LGGFTLPQLS IPAITTPAFT IDPIALGGFT LPQIMTPEIT TPPFAIDPIG LSGFTLPQVN 840
IPBITTPEFT IQPVGLAAFT TPALTIASIH LPSTTMGGFA IPAGPGYFNS SATPSLGFFN 900
35 AGIGGNSGFG NSGSGLSGWF NTSPVGLLAG SGYQNYGGLI SGFSNLGSGI SGFANTGTLT 960
FAVTSLVSGL ANIGNNLSGL FFQSTTP 987
<212> Type : PRT
<211> Length : 987
SequenceName : SEQ ID 153
SequenceDescription :
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Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
45 MSFVVVAPEV LAAAASDLAG IGSTLAQANA AALAPTTAVL AAGADEVSAA IASLFGAHGQ 60
AYQAVSAQMS AFHAQFMQAL TGAGGAYAAA EAVNVSAQNS VEQDLLAAIN ARFERIFGRP 120
LIGDGANGGP QDGGGPGGLL YGNGGNGGTS TTVGMAGNGG GAAGLIGNGG FGGGGGPGAA 180
GGNGGAGGWL FGNGGAGGAG GLGVAPGVPG GAGGAGGAGG VGGPAGLWGH GGAGGAGGAG 240
50 VAGAGGFEGT IGAGGAGGVG GAGGVGGAGG AGGWLYGDAG AGGDGGVGGA GGTGGLGNRG 300
GAGGAGGAGG VGGAGGAAGL WGGGGAGGVG GTGGGAGLGA QSVTFSSSLG GLSGGDGGAG 360
GAGGAGGAGG TGGWLYGGGG AAGSGGDGGT GGQGGAGGAG VFSLFGSGGG PGGNGGVGGV 420
GGVGGAGGRA GLFGVGLGG AGGDAGDSGE GGFGGPGLAG GLFGNPGNGG VGGIGGDAAG 480
GGAGGAGGNG GAGGNGGWL FNGGAGGSGG DGGAGAGGGA GNLGSAGGIN APAGNPGSGS 540
55 VGIGGAGGAG GTAGLFGDGG AGGAGGAGAA GGFGGISAA PSAGSEGAMG GAGGVGNAR 600
LLGTGGAGGV GGGGGAGGDG GRGGVATPGG QGGDAGDGA GAGGNGGGA SGAGGWLLGT 660
GGAGGAGGNG GNGKAGFSP GPTNFGLNGA GGGGVGGNG ATGPWLFGDG GPTPGSTGAG 720
AAGGHGGDAQ LIGNGGHGA GGTGVPNGSG GAGGLSGLLF GEPGANG 767
<212> Type : PRT
60 <211> Length : 767
SequenceName : SEQ ID 154
SequenceDescription :
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65 <213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

MSFVIANPEM LAAAATDLAG IRSAlSAATA AAAAPTlQVA AAGADEVSLA ISALFGQHAQ 60
AYQALSAQAT IFHDQFVQAL TSGGNLYAAA ESHTVEQMVL NAINAPTQTL FGRPLIGDGA 120
NGTAENPDGQ NGGLLFGNGG NGFTQTTAGV AGGNGGSAGL IGNGGAGGGG GAGAAGGLGG 180
5 NGGWLYGNGG AGGIGGAGTG TGGHGGAGGA GGRRAWLWGTG GAGGAGGDGG WLFQDGGAGG 240
TGGNGGSGFN SLTSSVGGAG GAGGHAGLFG AGGTGGTGGI GGQNTETGPA ASNGGAGGAG 300
GGGGYLVGDG GAGGTGGAGG KNSSGGATLT GGTGGTGGAG GAAGWLYGSG GAGGAGGAGG 360
LNNAGGATGG TGCTGGAGGS GAWLYGNGGA AGAGGNGGNN TSAGTGGVGA SGCTGGNAGL 420
IGAGGHGGAG GAGGNQTGGV GNGGAGGNGG AGGAGGQLYG NGGDGGNGGA GGANIAGGNG 480
SDGGAAGHGG AGGSARLIGA GGHGGDGGAG GNTAGRRADA IAGTGGDGGN GGNGLLSGN 540
10 AGAGGHGGAG GSSTATTTTG TPPTGATGGN GGNCGAGGTA GFTGSGGIGG NGGAGGTGGN 600
ACVALSVGST GGLGGNGGSG GLGGGGGSLF GNGGAGGVGA TGGNGGSGIG PASVGGNGGK 660
GGVGAAGGLA GQIGNGSGSG SGAGGNGGT GDTAGNGNG GAGAVGGNAQ LIGNGGNGGG 720
CGNGGTGADG T 731
<212> Type : PRT
15 <211> Length : 731
SequenceName : SEQ ID 155
SequenceDescription :

Sequence

20 <213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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NNIGFGNTGS GNFGFGNTGN NNIGIGLTGD GQIGIGGLNS GSGNIGFGNS GTGNVGLFNS 120
25 GTGNVGFNGS GTANTGFGNA GNVNTGFWNG GSTNTGLANA GAGNTGFFDA GNYNFGSLNA 180
GNINSSFGNS GDGNSGFLNA GDVNSGVGNA GDVNTGLGNS GNINTGGFNP GTLNTGFFSA 240
MTQAGPNSGF FNAGTNSGF GHNDPAGSGN SGTQNSGFNG SGYVNTSTTS MFGGNSGVLN 300
TGYNNSGFYN AAVNNTGIFV TGVMSGFFN FGTGNSGLLV SGNGLSGFFK NLF 354

30 <212> Type : PRT
<211> Length : 354
SequenceName : SEQ ID 156
SequenceDescription :

Sequence

35 <213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFVLAMPEV LGSAAATDLAA LGSVLGAADA AAAATTTGIV AAAQDEVSA IAALFSAHGR 60
40 AYQVASAQAA AVHAQFVEAL SAGACAYASA EAAGAAVLAN PAQSVQQDIL AAVNAQSVAL 120
TGRPLIGNGA NGAPGTGANG APGGWLLGNG GAGGSAAAGS GLPGGAGGAA GLFGTGGAGG 180
AGGSSTVGDG EAGGAGGSGG WLLGTGGVGG VGGLGAGAGG AGGVGGAGGL LGAGGHGGAG 240
GLGAVTGGVG GTGGAGLLA GLLAGPAGAG GTGGRGFLNN GGVGGAGGNA GLLFGAGGTG 300
GSGGAGLGGD GGAGGAGGNT GVLFNGAGSG GTGGFGDTDG CAGGAGGDAG WLGSAGVGG 360
45 GGFGETDGG VGGAGGKAGL LIGNGGAGGA GGQAVTGGT GGAGGDGVL I GNGGNAGIG 420
TGPTAGDTGA GGISGLLLGA DGFNTPASAS PLHTLKQQA AAINAPTQTL TGRPLIGNGT 480
PGAVSGGATG APGGWLLGDC GAGGSGAAGS GAPGGAGGAA GLWGTGGAGG AGGSSAGGGG 540
AGGAGGAGGW LLGDGGAGGI GGASTVLGGT GGGGGVGGW CAGGAGGAGG TGLVGGDGA 600
GGAGGTGGLL AGLIGAGGGH GGTGGLSTNG DGGVGGAGGN AGMLAGPGA GGAGGDGENL 660
50 DTGGDGGAGG SAGLLFGSGG AGGAGGFGFL GGDGAGGNA GLLLSGGAG GFGGFGTAGG 720
VGGAGGNAGW LGFGGAGGVG GSAGLIGTGG NGGNGGTGAN AGSPGTGGAG GLLLGQNGLN 780
GLP 783
<212> Type : PRT
<211> Length : 783
55 SequenceName : SEQ ID 157
SequenceDescription :

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60 <213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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QYQALSVQVA AFHEQFVQAL TAAAGRYAST EAAVERSLLG AVNAPTEALL GRPLIGNGAD 120
GTAPGQPGAA GGLLFGNGGN GAAGGFGQTG GSGGAAGLIG NGGNGGAGGT GAAGGAGGNG 180
65 GWLWNGCGNG GVGGSVAAG IGGAGGNGGN AGLFGHGGAG GTGGAGLAGA NGVNPTGPA 240
ASTGSPADV SGIGDQTGGD GGTGGHGTAG TPTGTTGGD ATATAGSGKA TGGAGGDGTT 300
AAAGGGGNG GDGGVAQDI ASAFGGDGGN GSDGVAAGSG GSGGAGGGA FVHIATATST 360

GGSGGFGGNG AASAASGADG GAGGAGGNGG AGGLLFGDGG NGGAGGAGGI GGDGATGGPG 420
GSGGNAGIAR FDSPDPEAEP DVVGGKGGDG GKGGSGLGVG GAGGTGGAGG NGGAGGLLFG 480
NGGNGGNAGA GGDGGAGVAG GVGNGGGGGG TATFHEDPVA GVWAVGGVGG DGGSGGSSLG 540
VGGVGGAGGV GKGKGASGML IGNGGNGGSG GVGAGAGVGG AGGDGGNGGS GGNASTFGDE 600
5 NSIGGAGGTG GNGGNGANGG NGGAGGIAGG AGGSGGFLSG AAGVSGADGI GGAGGAGGAG 660
GAGGSGGEAG AGGLTNGPGS PGVSGTEGMA GAPG 694
<212> Type : PRT
<211> Length : 694
SequenceName : SEQ ID 158
10 SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
15 <400> PreSequenceString :
MSFVIAAPEV IAAAATDLAS LESSIAAANA AAAANTTALL AAGADEVSTA VAALFGAHGQ 60
AYQALSAQAQ AFHAQFVQAL TSGGGAYAAA EAAATSPLLA PINEFFLANT GRPLIGNGTN 120
GAPGTGANGG DGGWLIIGNG AGGSGAAGVN GGAGNGGAG GLIGNGGAGG AGGRASTGTG 180
GAGGAGGAAG MLFGAAGVGG PGGFAAFAA TGGAGGAGGN GGLFADGGVG GAGGATDAGT 240
20 GGAGSGSNGG GLFGAGGTGG PGGFIFGGG AGGDGSGSGL FGAGGTGSGS GTSIINVGGN 300
GGAGSDAGML SLGAAGGAGG SGGSNPDGGG GAGGIGDGG TLFGSGGAGG VCGLGFDAGG 360
AGGAGGKAGL LIGAGGAGGA GGGSPAGAGG TGGAGGAPGL VGNAGNGGNG GASANGAGAA 420
GGAGSGSVLI GNGGNGSGSG TGAPAGTAGA GGLGGQLLGR DGFNAPASTP LHTLQQIILN 480
AINEPTQALT GRPLIGNGAN GTPGTGADGG AGGWLFNGG NGGHGATGAD GGDGSGSGAG 540
25 GILSGIGGTG GSGGIGTTGQ GGTGGTGGAA LLIGSGGTGG SGGFGLDTGG AGGRGGDAGL 600
FLGAAGTGGQ AALSQNFIGA GGTAGAGGTG GLFANGGAGG AGGFGANGGT GGNGLLFGAG 660
GTGGAGTLGA DGGAGGHGGL FGAGGTGGAG GSSGCTFGGN GSGGNAGLL ALGASGGAGG 720
SGGSALNVGG TGGVGGNGGS GGSLLFGFGA GGTGSSSIG SSGGTGGDGG TAGVFGNGGD 780
GGAGGFGADT GGNSSVPNA VLIGNGNGG NGCKAGGTPG AGGTSGLIIG ENGLNGL 837
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<212> Type : PRT
<211> Length : 837
SequenceName : SEQ ID 159
SequenceDescription :
35

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
40 <400> PreSequenceString :
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AYQAASAEAA AFHGRFVQAL TTGGGAYAAA EAAAVTPLLN SINAPVLAAT GRPLIGNGAN 120
GAPGTGANGG DAGWLIIGNG AGGSGAKGAN GGAGGPGGAA GLFGNGGAGG AGGTATANNG 180
IGGAGGAGGS AMLFGAGGAG GAGGAATSLV GGTGGTGGTG GNAGMLAGAA GAGGAGGFSF 240
STAGGAGGAG GAGGLFTTGG VGGAGGQGHG GGAGGAGGAG GLFGAGGMGG AGGFGDHGTL 300
45 GTGGAGGDGG GGGLFGAGGD GGAGGSLTT GGAAGNGGNA GTLSLGAAGG AGGTGGAGGT 360
VFGGKGGGAG GAGGNAGMLF GSGGGGGTGG FGFAAGGQGG VGSAGMLSG SGGSGGAGGS 420
GGPAGTAAGG AGGAGGAPGL IGNGGNGGNG GESGGTGGVG GAGGNAVLI NGGEGGIGAL 480
AGKSGFGGFG GLLLGADGYN APESTSPWHN LQDILSFIN EPTEALTGRP LIGNGDSGTP 540
GTGDDGAGG WLFNGGNGG AGAAGTNGSA GGAGGAGGIL FGTGGAGGAG GVGTAAGGA 600
50 GGAGGS AFLI GSGGTGGVGG AATTTGGVGG AGGNAGLLIG AAGLGGCGGG AFTAGVTTGG 660
AGGTGGAAGL FANGGAGGAG GTGSTAGGAG GAGGAGGLYA HGGTGGPGGN GGSTGAGGTG 720
GAGGPGGLYG AGGSGGAGGH GGMAGGGGGV GGNAGSLTLN ASGGAGGSGG SLSGKAGAG 780
GAGGSAGLFY GSGGAGNGG YSLNGTGGDG GTGGAGQITG LRSFGGAGG AGGASDTGAG 840
GNGGAGGKAG LYNGGDDGGA GGDGATSGKG GAGGNAVVI NGGNGGNAGK AGGTAGAGGA 900
55 GGLVLGRDQ HGLT 914
<212> Type : PRT
<211> Length : 914
SequenceName : SEQ ID 160
SequenceDescription :
60

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
65 <400> PreSequenceString :
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LIGDGAAGAP GTGQAGGAGG ILWNGGAGG SGAPGQVGA GGAAGLFGTG GAGGAGGAGA 180

AGGAGGSSGGW LLGNGGVGGA GGQSLGGAT GGAGGNAGLF GVGGTGGPGG PGGPGGVGGT 240
GGAGGLGGTL YGAGGHGGAG GPGPIGGVGG HGGVGGAGL LGVGGHGGAG GHGAEGVAGA 300
AGEDLSPHGT SGGVGGDAGD GGTGGRGGWL AGAGGAGCAG GVGGTGGAGG AGFSRALIVA 360
5 GDNNGDGGNG GMGGAGGAGG PGGAGGLISL LGGQGAGGAG GTGGAGGVGG DRGAGGPGNQ 420
AFNAGAGGAG GHGGDPGAGG AGGTGGAGSI TGAQGAIGAT PTSGGNGGAG GNGANATTAG 480
TNGANGGPGG HGGLVGNAGGA GGNANGAAG TNASDSGAVG GKGNSSGGNG QGGAGGDGGT 540
LAGNGGAGGT GCRGADGGLG GSGAEGANAT TAGERGQDGG KGGNGGVGGT GGNVAVPGAN 600
GGHGGNGGNP GFSGAGGLGG LSGDGVTRAA QGATPDFADT GKGKGGNGNG ANAVAPGGTG 660
ASGGAGGNAG AGGKGGENII GDGGGGNGGA GKGKGAGTLL GLTVFGDNNG AGVLGDSTDP 720
10 DSGGAGGAG GAGGAGDPT I 741
<212> Type : PRT
<211> Length : 741
SequenceName : SEQ ID 161
SequenceDescription :
15 Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
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IGNGANGTAA SPNGGDGGIL YNGGNGFSQ TTAGVAGGAG GSAGLICNGG NGGAGGAGAA 180
GGAGGAGGWL LGNGGAGGPG GPTDVPAGTG GAGGAGGDAP LIGWGGNGGP GGFAPFGNGG 240
AGNGGASGS LFGVGGAGGV GGSSEDDVGT GAGGAGGRGL FLGLGGDGA GGTNNNGGD 300
25 GGAGGTAGGR LFLSGDGGN GGAGTAIGSN AGDGGAGGDS SALIGYAQGG SGGLGGFES 360
TGGDGLGGA GAVLIGTVG GFGGLGGSN GTGGAGGAGG TGATLIGLGA GGGGGIGGFA 420
VNVNGVGGGL GQCGQGAAL IGLGAGGAGG AGCATVVLG GNGGDGGDG GLFSIGVGGD 480
GGNAGNGAMP ANGGNGGNAG VIANGSFAPS FVGFGNGGN GVNGGTGSG GILFGANGAN 540
GPS 543
30 <212> Type : PRT
<211> Length : 543
SequenceName : SEQ ID 162
SequenceDescription :
35 Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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GTNGAPGTGQ AGGPGGLLYG NGGNGSGGV GQAGGAGGSA GLIGIGGTGG AGGAGAVGGV 180
GGNGGWLYGN GGAGGLGGTG VAGVNGMGMA AGGAGGNAYL FGSGGAGGQG GMGAAGADGV 240
NPTPTGTADA GSTGTDQTLG GNAIGNGGP GDAGDAMTSG GAGSGGNAV STVNGDAVGG 300
EGKKGEGAY GGAGGAGGSA ASIGNAAIGG NGGAGGNAQA PGGVGGAGGE GGDQVGTNS 360
45 PSNAEAGNGG SGGNGFDSFA SGTGGAGGT GGAGGRGGLL IGDGGAGGAG GVGTTGSSGA 420
PGGGGGAGGD GGAANTDSAG SSRKAFGGDG GVGDDCASAL GTGEGGIGG QGGNGGAGGL 480
LIGNGGAGGV GGTAGAGGTG GSGGAGGAGG AGGGGTNSGP GAAPFGNGNT GNGGNGGAP 540
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SAGQPG 606
50 <212> Type : PRT
<211> Length : 606
SequenceName : SEQ ID 163
SequenceDescription :
55 Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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TYQALRTQAA AFHQIIVQTL TSTAGAYASA EAANVEQQLL GAINAPTMAI LGRPLIGHGA 120
DGAPGTGQAG GAGGILYNGG NGGSGGATGQ AGGAGGAAGL IGHGGAGGLG GTGASGGAGG 180
AGGWLWNGG AGNGGVGVVA GPPGVGGAG GAGGAAGLWG SGGSGGTGCG GGVGGKSGD 240
GGTGGIGGAG GGGWLHGDG GAGGHGGQGG TGVSSGGNGG AGGTGGDGRG LSGSGGAGGR 300
GGQTGVGGKV GBNFNGGAGG AGGTGGLIGN GGAGNGGQG AISGAGGAGG NAWLIGDGA 360
65 GNGGDIRGQ GGGAGGAGGA GGQLIGNGTT GGAGGTVTSP NGLGGAGGAG GSAGLIGHG 420
TGGAGGHSAG GPDGNGGI GG AGGAGGNGGQ LYGTGGTGGT GKGGDGFGV FGKGGAGGTG 480
GRGGAAGLIG DAGTGGTGGK GGTAGEDGTG GNGGTGGNGG AAVLIGNGGG GGAGGNGGAG 540

NDGTPGNGGG GGVGGTGGTL FGQPGQPGPP GQPGPA 576
<212> Type : PRT
<211> Length : 576
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5 SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
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QQAQELSAH AVAFHEQFVQ LMSAGAAQYA SAEANSSPL QIVGQTALDA INSPVQTLTG 120
RPLIGNGANG VAGTGQNGGD GGWLYGNNGN GSGSGTGQNG GNGGSAGLWG SGGNGGQGGG 180
GANGAAGQPG KAGGSGGNGG AGGWIYGHGG HGGAGGNGGM ATAPCGASAG FDGGACNNGG 240
15 SGGRGGLLFG NGGNGSVGGM GGQGTNDTAG DSAGSGGLGG NGGNGAQGGW LIGNGGQGGD 300
SGAGGTDST QTGVMNAGSG GSAGIAGNGG DAGLVNGGA GNGGNGAAG SALGTTIFGG 360
SGGVGGSGGD GNGGWLFGS GASGNGGQG GDAGTNGFAG FGGSAGGGGW VGAVNFGPI 420
VQGFGLFHHG GDGGNGGDDV AGSLSIQFGA SGGDGGQGGV LYNGGNGNGN AGSGGGTGFE 480
GSAGQGGAAI LIGNGGAGGN GATGTTGVGN IIQEAGDGS DGGAGGSGGL LFGSGGAGGI 540
20 GGAGGVGGSG NDGGNGGDDG QGGASGLGIG NGGPGSGSGT GGAGGTGSSA GTGGAGGDDG 600
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<212> Type : PRT
<211> Length : 639
SequenceName : SEQ ID 165
25 SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
30 <400> PreSequenceString :
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GAPGTGANGG PGGWLIENG GAGSGAPGAG AGGNGGAGGL FGSGGAGGAS TDVAGGAGGA 180
GGAGGNAGML FGAAGVGGVG GFSNGCATGC AGGAGGAGGL FGAGRERGS GSGNLTGGAG 240
35 GAGGNAGTLA TGDGGAGGTG GASRSGGFGG AGGAGGDAGM FFGSGGSGGA GGISKSVGDS 300
AAGGAGGAPG LIGNGGNGCN GCASTGGGDG GPGCAGGTGV LIGNGGNGGS GGTGATLGKA 360
GIGGTGGVLL GLDGFTAPAS TSPLHTLQD VINMVNDPFQ TLTGRPLIGN GANTPTGTGA 420
DGGAGGWLFG NGGNGGQGTI GGVNGGAGGA GGAGGILFGT GGTGSGGGPG ATGLGGIGGA 480
GGAALLFGSG GAGGSGGAGA VGGNGGAGGN AGALLGAAGA GGAGGAGAVG GNGGAGGNGG 540
40 LFANGGAGGP GGFSGPAGAG GIGGAGGNGG LFGAGGTGGA GGGSTLAGGA GGAGNGGLF 600
GAGGTGAGS HSTAAGVSGG AGGAGGDAGL LSLGASGAG GSGGSSLTAA GVVGGIGGAG 660
GLLFGSGGAG GSGGFSNSGN GGAGGAGGDA GLLVGSGGAG GAGASATGAA TGGDGGAGGK 720
SGAFGLGGDG GAGGATGLSG AFHIGGKGGV GGSAVLIGN GNGGNGNSG NAGKSGGAPG 780
PSGAGGAGGL LLGENGLNGL M 801
45 <212> Type : PRT
<211> Length : 801
SequenceName : SEQ ID 166
SequenceDescription :

50 Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
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55 GADGASGPVG QPGGDGILW GNGGNGDST SPGVAGGAGG SAGLIGNGGR GGNGAPGGAG 120
GNGGLGGLL GNGGAGGVGG TGDNGVGD LG AGGGGGDGL GGRAGLIGHG GAGGNGGDDG 180
HGGSGKAGGS GSGGFGQFG GAGGLLYNG GAAGSGNGG DAGTGVSSDG FAGLGGSGGR 240
GGDAGLIGVG GGGGNGGDP GLGARLFQVG SRGGDGGVGG WLYGDGGGGG DGGNGGLPFI 300
GSTNAGNGGS ARLIGNGGAG GSGSGAPGS VSSGGVGGAG NPGSGGNGG VWYNGGAGG 360
60 AAGQGGPGMN TSPGGPGGV GGHGGTAILF GDGGAGGAGA AGGPPTPDGA AGPGGSGGTG 420
GLLFGVPGPS GPDG 434
<212> Type : PRT
<211> Length : 434
SequenceName : SEQ ID 167
65 SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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PASAAMAAAA APYAGFLTTA SAQAQLAAGQ AKAVASVFEA AKAAIVPPAA VAANREAFLA 120
LIRSNWLGLEN APWIAAVESL YEEYWAADVA AMTGYHAGAS QAAAQLPLPA GLQQFLNTLP 180
NLGIGNQCGNA NLGGGNTGSG NIGNGNKGSS NLGGGNIGNN NIGSGNRGSD NFGAGNVGTG 240
NIGFGNQGP I DVNLLATPGQ NNVGLGNIGN NNMFGFNTGD ANTGGGNTGN GNIGGGNTGN 300
NNFGFGNTGN NNIGIGLTGN NQMGINLAGL LNSGSGNIGI GNSGTNNIGL FNSGSGNIGV 360
10 FNTGANTLVP GDLNNLVGNG SGNANIGFGN AGVLNTGFGN ASILNTGLGN AGELNTGFGN 420
AGFVNTGFDN SGNVNTGNGN SGNINTGSWN AGNVNTGFGI ITDSGLTNSG FGNTGTDVSG 480
FFNTPGTPLA VDVSGFFNTA SGGTVINGQT SGIGNIGVPG TLFSGSVRSL NTGLFNMGT 540
ISGLFNLRL LG 552
<212> Type : PRT
15 <211> Length : 552
SequenceName : SEQ ID 168
SequenceDescription :

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<400> PreSequenceString :
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AYQALSAHVA AFHDQFVHTL TAGAGSYMAA EAAAASPLQA LQLELLNAIN APTLALLGRP 120
LIGDGTDAAP GSGGAGGAGG ILIGNGGTGG ASDLAGTGRG GVGAGGAGG LFGIGGAGGG 180
CGSAVAIGGD GGAGGAGGVF SGGGAGGAGD AIGGSGGAGG TGGLLGGGGG AGGAGGAGGN 240
GGGASNSASI GGDGGSGGAG GMLYGAGGVG GNGGAAVAIG GDGGAGGRAG AIGNGGDGGN 300
GGTSNTPGGS GGDGGNGGNA GLIGNGGNGG NAEIVISGGS VAGTGGNGGL LLGPNGTNGL 360
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<211> Length : 361
SequenceName : SEQ ID 169
SequenceDescription :

Sequence
35 -----
<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
40 AQASPAAHGG SGGAGGNGGA GSAGNGGAGG AGGNGGAGGN GGGGDAGNAG SGGNGGKGGD 60
GVGPGSTGGA GKGKGAGANG GSSNGNARGG NAGNGGHGGA GSGGDTGGAG GAGGQGGFGG 120
TGGSGSGIGG GAGGNGGNGG AGGTGVVLGG KGGDGGNGDH GGPATNPGSG SRGGAGGSGG 180
NGGAGGNATG SGGKGGAGGN GGDGSFGATS GPASIGVTGA PGGNGGKGGGA GGSNPNSSGG 240
DGGKGGNGGA GGNNGSIGAN SGIVGGSGGA GGAGGAGNG SLSSGEGGKG GDGGHGGDGV 300
GGNSSVTQGG SGGGGGAGGA GSGGFFGGKG GFGGDGGQGG PNGGGTVGTG AGGGGNGGVG 360
45 GRGDGVFAG AGQGGGLGGQ GGNNGGSTG NGGLGGAGG GGNAPDGGFG GNGGKGGQGG 420
IGGGTQSATG LGGDGGDGGD GNGNGNSGAK AGGAGGKGQA GQPNSTGTEPG FGGDGGGLGA 480
GATP 484
<212> Type : PRT
<211> Length : 484
50 SequenceName : SEQ ID 170
SequenceDescription :

Sequence
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<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
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GGREIKISAD KANAIIGGIN TLKELPDFGG VEVSONVSIG PLNAGEDLNT NFGPLKFISN 120
NVTSIITGVG TKTFNSNIDFA GKNA TLQINK DLNITTKIDN TVAGNNGSIT FEGSGIISNH 180
60 IGYTNSLLGI NVNGEAKIY APEANNITIN AKNINLTHNN SILTLCDGNI TTLKGNINNT 240
TEIDGQGLN LAYDLGSSSI ITGDIIGNIGS LDTINVLLGS ATFNSTILKA TNINLKHNTS 300
TLNLDNIIIV IGNIKGNNNK DILNFKVHGT NLDNEMIIPA POKTHGTINF KGNATLNGNI 360
NNLNILKFSG GHGKTLNLQG NTKVDNLVFA DSVLDSGTIS VNGLLDTCV TFNNSNVNNG 420
TLIINAKNTI SAKLLNATKA KIQINANLTM NHPSAGDISD IRIADNTIYT IDAKNGNVNL 480
65 LNNNAKIIFE GADSMALIN TGVTDADTFT IYNNLNQSGN DEYGIVKIEA IKKVITIANQ 540
SGPYTIQDN THRLKELIVE GAGDIIIDDT IFTKLLSINS TGQITFNRTL DLGAGGNIAF 600
GKHGTLVVNG VTGSITTSEN NQGILTINS NITGVIGTNE LGLKLVNIGA DPVTCSANVF 660

	ASVALTNPSS	VLILADGVTL	TGEVTTNNNT	KGVLSLGTGS	NITQIGTNS	AALKINIGA	720
	GASNIDSNIY	AGSTVLTDQT	SELTNNNDVV	VNSNIITTAG	NNSGKLITG	NGGITGNIGA	780
	NGAALQEVVF	NGTTNIGGTA	NSQFTVAHS	AANVVITGLT	TGALKYKDTG	TIIAHGGLVG	840
	DIDFNNKAGK	FILGDBGAMID	GSVLCNGGVA	GTLDFIGDGN	VTQNIAGDNA	NSISTINIQQ	900
5	DNTKNTVIAN	DIFVDNIHFT	NGGILQLGCG	LTTHNIDFGA	NGGTLEFNGN	NTYNLNAIIV	960
	NGQNGILNAF	TNLKASDDTI	GTVKIINIGQ	IGTPQNFTIQ	VNNKNLTLVS	SVNSSINFGD	1020
	ANSQILLSAP	VDQTIKFINN	LNETGGGIIIT	LDSNGNNLTI	SGNNGIKLGS	KGNELSSLNI	1080
	KGKVTVTNDL	DIQNIHQNLN	NNGALFDDQS	LTSKIKININ	IGTVAGGATY	TLDAINDNFD	1140
	LNTSGMVFKH	QDSILELKNS	SNNDHTITL	TSALDPGNNQ	FGTIKLITDT	NKLTIDNNGN	1200
10	VAYTLGTANH	MLKQLTFASI	DNGAIALKVG	INVENVTLNI	KDIELNEVNA	NVLFNKNTTY	1260
	TATGNINGHV	DFQGNAGVIN	LNDIEIDGS	VTSTGNVNGT	LNFGSGKVT	GLINNIVMLQ	1320
	AGAGDVLSLA	SGNYSITEIQ	GNGNNNLTF	ANSHLTTDIN	KTGGQDLNLV	FINGGSSVGS	1380
	IGANAAGVDI	IINAGSVNFS	NTLKSGNIVI	SDGATMQVNN	NVTATDISGK	NANNGLTKLN	1440
	NHTPINITST	IGNNNAIGTI	EVANNDVTIT	GTLQAQNIHF	SNATQAATLT	LGAASQVTNI	1500
15	TTAGNNIHTL	EVTDFDTGND	GIIGDANNRL	KSIELTGNGT	VTINSPHVYS	SITTANNAQG	1560
	NVKLNIEGGI	TYDLGSKIKS	LANVQISED	TIRGDVYSKY	LNIDAGKTIN	PDRGDNNMNP	1620
	KNLDIPDALI	DLDDVLPRLS	LFNYFTDIIA	DNLNFPADDTA	TANFKDAVVI	DAHIDNGGIL	1680
	KFNDNAWLTQ	EIKNANIEI	ASDKFMLLQK	NIKAATLIAD	NANLVLLDNV	EVNTNLNVRD	1740
	IVLDLANYEL	KYTGNVTHNG	LLTIITYFDT	ALQKGGHILV	SQGSNVDMSD	LDNLIIKKA	1800
20	HSIDITNITS	TKHQIVKLET	GAITYPVPQT	KVIIDASEEQ	NKFVKWVADA	NGLVLLTDTG	1860
	GRDDTGGRDD	TRGRGNTDNG	CRDNCVGN	SNSSNEAGG	SSSDKNYGIT	DVVPIDFDPSP	1920
	ILDYTKNNYV	ASGIANQLIN	HVKDFGNTTD	AGKLLNDLGF	MSPNRVTETL	DRLSNRINVN	1980
	GLNEGVVGLN	GIEVENFLTD	IATNMDNFTA	KEIGNRLEEL	SDANTVNGLN	KTNTLLNNKI	2040
	NLKRNLNTNN	AIIAAGDEDN	IVTGIWGMSE	YGKIKQNSKN	SASGYQSNTG	GGIIGFDYNI	2100
25	DNSIVTGAAY	TMAADSKVHK	NDKNGDRTKA	KSNYSIYGL	YNWLTNNFFV	BAIGVYGRNK	2160
	IKNYEKRIIT	ITDQIAIGKF	INTFYSYELL	GGYNYLISHR	TTITPMFGMR	YATFKNNGYK	2220
	ENNTTFQNL	IKKNYYDKFE	TILGLNSVTH	YLSQDIIKIP	ELHWFINYQC	KNKLPNIDAR	2280
	LDGIDEPLTT	IRFKPAKITY	NLGGGISTKN	NMIEFGIRYN	LSLAKKYTAH	QGSCLKIKVNL	2340
30	<212> Type : PRT						
	<211> Length : 2340						
	SequenceName : SEQ ID 171						
	SequenceDescription :						
35	Sequence						

	<213> OrganismName : Rickettsia prowazekii						
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	ANIPVAPNSV	ITANANNPIT	FNTPNGHLNS	LFLDTANDLA	VTINEDTTLG	FITNIAQQAQ	120
	FFNFVTAAGK	ILNITGQGIT	VQEASNTINA	QNALTKVHGG	AANANDLSG	LGSITFAAAP	180
	SVLEFNILNP	TTQEAPLTG	ANSKIVNGGN	GTLNITNGFI	QVSDNTFAGI	KTINIDDCQG	240
	LMFNSTPDAA	NTLNQLVGGN	TINFNGIDGT	GKLVLVSKNG	AATEFNVGTG	LGNNLKGII	300
	LNTAAVAGKL	ISQGAANAV	IGTDNGAGRA	AGFIVSVDN	NAATISGQVY	AKNMVIOQAN	360
45	AGGQVTFEHI	VDVGLGGTTN	FKTADSKVII	TENSNGGSTN	FGNLDQIIVV	PDTKILKGNF	420
	IGDVKNNGNT	AGVITFNANG	ALVSASTDPN	IAVTNINAIE	AEGAGVVELS	GIHIAELRLG	480
	NGGSIFPKLAD	GTIVNGPVNQ	NALMNNNALA	AGSIQLDGSA	IITGDIGNGG	VNAALQHITL	540
	ANDASKILAL	DGANIIGANV	GGAIHFQANG	GTIKLTNTQN	NIVVNFDDI	TDDKTGVVDA	600
	SSLTNNQTLT	INGSIGTVVA	NTKTLAQLNI	GSSKTILNAG	DVAINELVIE	NNGSVQLNHN	660
50	TYLITKTINA	ANQGQIIVAA	DPLNTNTTLA	DGTNLGSAEN	PLSTIHFATK	AANADSILNV	720
	GKGVNLYANN	ITNDANVGS	LHFRSGGTSI	VSGTVGGQQG	HKLNNLILDN	GTIVKFLGDT	780
	TFNGGKIEG	KSILQISNNY	TTDHVESADN	TGTTLEFVNTD	PITVTLNKQG	AYFGVLKQVI	840
	ISGPGNIVFN	EIGNGVIVHG	IAANSISFEN	ASLGTSLFLP	SGTPLDVLT	KSTVNGTVD	900
	NFNAPIVVVS	GIDSMINNGQ	IIGDKKNIIA	LSLGSNDSIT	VNANTLYSGI	RTTKNNQGT	960
55	TLSGGMPPNP	GTIYGLGLEN	GSPKLKQVTF	TTDYNLNGSI	IANNVTINDY	VTLTTGGIAG	1020
	TDFDAKITLG	SVNGNANVRF	VDSTFSDPRS	MIVATQANKG	TVTYLGNALV	SNIGSLDTPV	1080
	ASVRFNGNDS	GAGLQGNIS	QNIDFGTYNL	TILNSNVILG	GGTTAINGEI	DLTNNLIFA	1140
	NGTSTWGDNT	SISTTLNVSS	GNIGQVVAE	DAQVNATTG	TTTIKIQDNA	NANFSGTQAY	1200
	TLIQGGARFN	GTLGAPNFAV	TGSNIFVKYE	LIRDSNQDYV	LTRTNDVLNV	VTTAVGNSAI	1260
60	ANAPGVSQNI	SRCLESTNTA	AYNNMLLAKD	PSDVATFVGA	IATDTSAAVT	TVNLNDTQKT	1320
	QDLLSNRLGT	LRYLNSAETS	DVAGSATGAV	SSGDEAEVSY	GVWAKPFYNI	AEQDKKGGIA	1380
	GKAKKTGVV	VGLDTLASDN	LMIGAAIGIT	KTDIKHQDYK	KGDKTIDINGL	SFSLYGSQQL	1440
	VKNFFAQGNA	IFTLNKVKSK	SQRYFFESNG	KMSKQIAAGN	YDNMTFGGNL	IFGYDYNAMP	1500
	NVLVTPMAGL	SYLKSSNENY	KETGTTVANK	RINSKFSDRV	DLIVGAKVAG	STVNITDIVI	1560
65	YPEIHSFVVH	KVNGKLSNSQ	SMLDGQTAPF	ISQPDRTAKT	SYNIGLSANI	KSDAKMEYGI	1620
	GYDFNSASKY	TAHQGTLLKVR	VNF				1643
	<212> Type : PRT						

<211> Length : 1643
SequenceName : SEQ ID 172
SequenceDescription :

5 Sequence

<213> OrganismName : Porphyromonas gingivalis W83

<400> PreSequenceString :

MARIILEAHD	VWEDGTGYQM	LWDADHNQYG	ASIPSEESFWF	ANGTIPAGLY	DPFEYKVPVN	60
ADASFSPTNF	VLDGTASADI	PAGTYDYVII	NPNPGLIYIV	GEGVSKGNDY	VVEAGKTYHF	120
TVQRQPGDA	ASVVVTGEGG	NEFAPVQNLQ	WSVSGQTVTL	TWQAPASDKR	TYVLNESFDT	180
QTLPLNGWTMI	DADGDGHNWL	STINVYNTAT	HTGDGAMFSK	SWTASSGAKI	DLSPDNYLVT	240
PKFTVPENGK	LSYVWSSQEP	WTNEHYGVFL	STTGNEAANF	TIKLEETLG	SGKPAPMNLV	300
KSEGVKAPAP	YQERTIDLISA	YAGQQVYLAF	RHFVGTGIFR	LYLDDVAVSG	EGSSNDYTYT	360
15 VYRDNVVIAQ	NLTATTFNQE	NVAPGQYNYC	VEVKYTAGVS	PKVCKDVTVE	GSNEFAPVQN	420
LTGSAVGQKV	TLKWDAPNGT	PNPNPGTTTL	SESFENGIPA	SWKTIDADGD	GNNWTTTPPP	480
GGSSFAGHNS	AICVSSASYI	NFEGPQNPND	YLVTPELSLP	NGGTLTFWVC	AQDANYASEH	540
YAVYASSTGN	DASNANALL	EEVLTAKTIV	TAPEAIRGTR	VQGTWYQKTV	QLPAGTKYVA	600
FRHFGCTDFF	WINLDDVEIK	ANGKRADTFE	TFESSTHGEA	PAEWTTIDAD	GDGQGWLCLS	660
20 SGQLGWLTAH	GGTNVVASFS	WNGMALNPDN	YLISKDV TGA	TKVKYKYAVN	DGFPGDHYAV	720
MISKTG TNAG	DFTVVFEETP	NGINKGGARF	GLSTEANGAK	PQSVWIERTV	DLPAGTKYVA	780
FRHYNCSDLN	YILLDDIQFT	MGGSPPTDID	TYTVYRDGTR	IKLEGLTETTF	EEDGVATGNH	840
EYCVKVKYTA	GVSPKECVNV	TVDPVQFNPV	QNLTGSAVQ	KVTLKWDAPN	GTPNPNP GTT	900
TLSESFENGI	PASWKTIDAD	GDGNNWTTTP	PPGGTSFAGH	NSAICVSSAS	YINFEGPQNP	960
25 DNYLVTPELS	LPNGGTLTFW	VCAQDANYAS	EHYAVYASST	GNDASNFA	LLEEVLTAKT	1020
VVTAPEAIRG	TRVQGTWYQK	TVQLPAGTKY	VAFRHFCTD	FFWINLDDVE	IKANGKRADF	1080
TETFESSTHG	EAPAEWTTID	ADGDGQGWLC	LSSGQLDWT	AHGGTNVVAS	FSWNGMALNP	1140
DNYLISKDVT	GATKVKYKYA	VNDGFPDGHY	AVMISKGTGN	AGDFTVVFEE	TPNGINKGGA	1200
RFGLSTEANG	AKPQSVWIER	TVDLPAAGTKY	VAFRHYNCSD	LNYILLDDIQ	FTMGGSPPTP	1260
30 DTYTVYVRDG	TKIKEGLTET	TFEEDGVATG	NHEYCVKVKY	TAGVSPKECV	NVTVDVPVQFN	1320
PVQNLTGSAV	GQKVTWKWDA	PNGTPNPNP	TTLSESFEN	GIPASWKTID	ADGDGNNWTT	1380
TPPPGGTSFA	GHNSAICVSS	ASYINFEGPQ	NPDNYLVTPE	LSLPNGGTLT	FWVCAQDANY	1440
ASEHYAVYAS	STGNDASNFA	NALLEEVLTA	KTVVTAPEAI	RGTRVQGTWY	QKTVQLPAGT	1500
KYVAFRHFCT	TRDFWINLDD	VEIKANGKRA	DFTTFESST	HGEAPAEWTT	IDADGDGQGW	1560
35 LCLSSGQLGW	LTAHGGTNV	ASFSWNGMAL	NPDNYLISKD	VTGATKVKY	YAVNDGFPD	1620
HYAVMISKTG	TNAGDFTVVF	EETPNGINKG	GARFGLSTEA	NGAKPQSVWI	ERTVDLPAGT	1680
KYVAFRHYNC	SDLNYILLDD	IQFTMGGSP	PTDYTYTVYR	DGTKIKEGLT	ETTFEEDGVA	1740
TGNHEYCVVE	KYTAGVSPKE	CVNVTINPTQ	FNPVQNLTA	QAPNSMDAIL	KWNAPASKRA	1800
EVLNEDFENG	IPASWKTIDA	DGDGNNWTTT	PPPGSSSFAG	HNSAICVSSA	SYINFEGPQNP	1860
40 PDNYLVTPEL	SLPGGTLTF	WVCAQDANYA	SEHYAVYASS	TGNDASNAN	ALLEEVLTA	1920
TVVTAPEAIR	GTRVQGTWYQ	KTVQLPAGTK	YVAFRHFCT	DDFWINLDDV	VITSGNAPS	1980
TYTIYRNTQ	LASGVTTETTY	RDPDLATGFY	TYGVKVVYPN	GESAIETATL	NITSLADVTA	2040
QKPYTLTVVG	KTITVTCQGE	AMIDYMNRR	LAAGRNTVYV	TAQGGHYAVM	VVVDGKSYVE	2100
KLAVK						2105

45 <212> Type : PRT
<211> Length : 2105
SequenceName : SEQ ID 173
SequenceDescription :

50 Sequence

<213> OrganismName : Porphyromonas gingivalis W83

<400> PreSequenceString :

MKTSERILSY	FFLLCAVFSL	GSCEGLYAQV	TFPNYSPTAA	SSIAVCSGEE	TLIIDFTVVQ	60
55 EDSNGIKVNV	KLADGVEYV	GTAVVSVTQG	NAVTVAEINV	SNPNEPVFTV	KSADGNNVVE	120
LGTIVKLTIK	RRAVCTAWSN	AINAAETGFV	FKDKVTVTIG	DHSDSKESNS	YSVNYPNLTI	180
KQPAPQVKNQ	IGETIVREFS	ITNGSQNPQT	TVYLSIEYPD	EAYLTGVGAM	TLQAKLGASG	240
TYADLTPTVT	NGKVRIYTLS	GSSLGPDHLL	TNGEIIYLYE	TFKLKTCAPV	TVYRVGWGCS	300
IDSQCEIKTT	AATITMAAGA	ANITGYSVTG	PDYRSPTFSL	CQPFELTIKF	SNSGAGGSMG	360
60 AAFNINTIGR	NDYYRPRGFV	LHEFIDVKNV	GKPVNTFKTD	GSELDLRFDG	QFTEDPDGPG	420
VGLDDVDGDG	FYDDLPGVAT	ITITVTVRLK	CDQFTACNNA	PNDLSDRGLI	LKTLYQTSCT	480
RTSWIDPNTW	RLSSSTHLYL	SRESVQDASH	MPTVIEKDTF	FDLKIMTSY	SILSSYNNIW	540
YANPNTRYV	EIVFPQGMTM	PPKSDIEWTN	IKNHPIDGSL	VFTPPINLDP	ANITTSNGTM	600
TIVSPSQERG	FVTLHGVKYD	CTNNHEMVVE	YKIREVFNYL	HFPDCLCPVG	PIMCNTAKRY	660
65 VLGDPPCGR	GAETSVPKIE	RADNSLGWTD	YTMRTQSR	NISAYDLAKA	LYMDEVNITA	720
TSIQHGTAASS	LGARFVLATG	VDRVETLTPL	SADIKIFRDG	VQIVSVVGYT	TFRSIRNNNN	780
AEQVIDWDF	SILPAGLLD	RDKVDVVTRY	RVTSONAHRV	DTQVGREWFF	YNSTANVSPI	840

	WDEANPLTCL	ILVPEIYIMG	TFVVNGTDPH	VISQCTPTDL	GRVANHYARR	FGSGAFEYAN	900
	EYRPGVKIRN	IYLVKPKSYT	LNKVEYSNHR	NHSSLGTTMP	FEEINHTDVT	SQGEYNIYKY	960
	QLADNEKAHF	NITVKNAIGA	ALKVNVSPCT	ASSAVATNYD	KISYYVDYID	YYYYAATQPT	1020
	VPNSLDIVAD	QSAGSNGIYS	VSALNVYNRP	ILYTNKPSIA	LVNQSSEVEL	VGKTGEWKLR	1080
5	ISNPSSATAP	YVWLALPTTS	GLTIEKVDA	AGTEMAFTTY	SGGKMYRLSE	AGVPVGSALD	1140
	YTIHFTYSGC	SPIALKAMGG	WNCSAYPLSL	DEVVCSQVI	DLKLKPLPAA	MELTEIAVPD	1200
	PTAAATLCST	LEYIYSIQST	DNANVYSPTF	SIFPEEGLVV	TPNQVQVEYP	AGSGNWAALN	1260
	VVNNSVNLLQ	HPALTITIGYL	KGLKEGESND	NQRKILVKFY	IKTECSFVSG	KNFRVRADGR	1320
	NACNQNAKGS	GLAISTPPIR	INGAIEPYTT	SASTQLVTTT	TSQSDCKAPK	RVKVVQTVVG	1380
10	GETTPKAYLE	ITLPLGFKYV	TGSYAPDNTH	PGGVNASPAG	TEEVTLTANG	EDKIKINVKA	1440
	GLTSGQSFAY	TLEMKEDDDN	VPACGNHTIE	IVNVEEIEGL	WCEGVQCAET	LVVTGANKFE	1500
	FELDKPYLDI	TVISAVSTFS	GGKENLTIEY	KVSNTSTTQP	LKPGAVVTLF	SDKDNNQVFS	1560
	GGDVAVATQE	LVAEITNTTP	LTQIMKVKGV	SSSHTGNLVL	TILPKDGCYC	EIKSPMVTLN	1620
	HLSPNYSGAN	TVGKPNWEKE	PNNWYNDQVP	DAEDEVFAT	EVNNPTDPNN	PKSGPAKENL	1680
15	HLDDIHQNGT	AGRVIGNLIN	DSKDLVITT	GNQLTINGVV	EDNNPNVGTI	VVKSSKDNPT	1740
	GTLLFANPGN	NQNVGGTVEF	YNQGYDCADC	GMYYRSWQYF	GIPVNESDFP	YDHDVGNATV	1800
	NQWVEPFNGD	KWRPAPYAPD	TKLQKFKGYQ	ITNDVQAQPT	GVYSFKGTLC	VCDAPLNLTR	1860
	TSGVNYSGAN	LIGNSYTGAI	DIKQGIYFPP	EAQIVVYLFN	TGTRDQWRKL	NGSTVSGYRA	1920
	GQYLSVPKNT	AGQDNLPDRI	PSMHSFLVKM	QNGASCTLQI	LYDKLLKNTT	VNNGNGTQIT	1980
20	WRSNGSGSAN	MPSLVMDVLG	NESADRLWIF	TDGGLSFGFD	NGWDGRKLTE	KGLSGLYAMS	2040
	DIGNDKFQVA	GVPELNNLLI	GFDADKDGQY	TLEFALSDHF	AKGGVFLEDL	SRGVTRRVVD	2100
	GGSYSFDAKR	GDGSGARFRLS	YDEEWVESAE	VSVLVGTACK	RIVITNNSEH	ACQANVYTTD	2160
	GKLLIRLDVK	PGSKSMTEPL	VDGVYVVSLO	SPATSSNVRK	VVVN		2204
	<212> Type : PRT						
25	<211> Length : 2204						
	SequenceName : SEQ ID 174						
	SequenceDescription :						
	Sequence						
30	-----						
	<213> OrganismName : Porphyromonas gingivalis W83						
	<400> PreSequenceString :						
	MNKFYKSLQ	SGLAASFVMA	TALTASAQIS	PGGEPLSFSS	RSAGTHSFDD	AMTIRLTPDF	60
	NPEDLIAQSR	WQSQRDGRPV	RIGQVIPVDV	DFASKASHIS	SIGDVDVYRL	QFKLEGAKAI	120
35	TLYYDAFNIP	EGGRLYIYTP	DHEIVLGAYT	NATHRRNGAF	ATEPVPGSEL	IMDYEVSRGG	180
	TLPDIKISGA	GYIFDKVGR	PVTDNHYGIG	EDDSDSDCIE	NINCEGADW	QAEKNGVQM	240
	IMVKGQYISM	CSGNLLNNTK	GDFTPLIISA	GHCASITTNF	GVTQSELDKW	IFTFHYEKR	300
	CSNGTLAIFR	GNSIIGASMK	AFLPIKGSKD	GLLQLNDEV	PLRYRVYNG	WDSTPDIPSS	360
	GAGIHHAPAGD	AMKISILKKT	PALNTWISSS	GSGGTDDHFI	FKYDQGGTEG	GSSGSSSLFNQ	420
40	NKHVVGTLTG	GAGNCGGTEF	YGRNLNHWNE	YASDGNTRM	DIYLDPQNNG	QTTILNGTYR	480
	DGYKPLPSVP	RLLLQSTGDQ	VELNWTAVPA	DQYPPSSQVE	YHIFRNGKEI	ATTKELSYSD	540
	AIDESIIGSG	IIRYEVSAF	IYPSPLDGVE	SYKDTDKTSA	DLAIGDIQTK	LKPDVTPPLG	600
	GGVSLSWKVP	FLSQLVSRFG	ESPMPVFKTF	EVPIVSAAAA	QTPNPPVGVV	IADKFMAGTY	660
	PEKAAIAAVY	VMPAPDSTF	HLFLKSNTR	RLQKVTTTSD	WQAGTWLRIN	LDKPPFPVND	720
45	HMLFAGIRMP	NKYKLNRAIR	YVRNPDNLFS	ITGKKISYNN	GVSFEGYGIP	SLLGYMAIKY	780
	LVTNTDAPKI	DMSLVQEPYA	KGTNVAPFPE	LVGIYVYKNG	TFIGTQDPSV	TTYSVSDGTE	840
	SDEYEIKLVY	KSGSISNGVA	QIENNNNAVVA	YPSVVTDRFS	IKNAHMHVAA	ALYSLDGGKQV	900
	RSWNNLRNGV	TFSVQGLTAG	TYMLVMQTAN	GPVSQKIVKQ			940
	<212> Type : PRT						
50	<211> Length : 940						
	SequenceName : SEQ ID 175						
	SequenceDescription :						
	Sequence						
55	-----						
	<213> OrganismName : Porphyromonas gingivalis W83						
	<400> PreSequenceString :						
	MKNLNKFVSI	ALCSSLLGGM	AFAQQTTELGR	NPNVRLLEST	QQSVTKVQFR	MDNLKFTEVQ	60
	TPKGMQAVPT	YTEGVNLSEK	GMPTLPILSR	SLAVSDTREM	KVEVVSSKFI	EKKNVLIAPS	120
60	KGMIMRNEDP	KKIPYVYGKS	YSQNKFFPGE	IATLDDPFIL	RDVRGQVNF	APLQYNPVTK	180
	TLRIYTEITV	AVSETSEQGK	NILNKKGTFA	GFEDTYKRMF	MNYEPGRYTP	VEEKQNGRMI	240
	VIVAKYEGD	IKDFVDWKNQ	RGLRTEVKVA	EDIASPVTAN	AIQQFVKQEQ	EKEGNDLTYV	300
	LLIGDHKDIP	AKITPGIKSD	QVYQIVGND	HYNEVFIGRF	SCESKEDLKT	QIDRTIHYER	360
	NITTEDKWL	QALCIASAEG	GPSADNGESD	IQHENVIANL	LTQYGYTKII	KCYDPGVTPK	420
65	NIIDAFNGGI	SLANYTGHS	ETAWGTSHFG	TTHVKQLTNS	NQLPFIEDVA	CVNGDFLFMS	480
	PCFAEALMRA	QKDGKPTGT	ALIASTINQS	WASPMRGQDE	MNEILCEKHP	NNIKRTFGGV	540
	TMNGMFAMVE	KYKKGDEKML	DTWTVFGDPS	LLVRTLVPK	MQVTAPAQIN	LTDASVNVSC	600

DYNGAIATIS ANGKMFSGSAV VENGATATINL TGLTNESTLT LTVVGYNKET VIKTINTNGE 660
PNPYQPVSNL TATTQGGQVKT LKWDAPSTKT NATNTTARSV DGIRELVLLS VSDAPELLRS 720
GQAEIVLEAH DVWNDGSGYQ ILLDADHDQY GQVIPSdTHT LWPNCVSPAN LFAPFEYTVP 780
ENADPSCSPT NMIMDGTAHV NIPAGTYDFA IAAPQANAKI WIAGQGPTKE DDYVFEAGKK 840
5 YHFLMKKMGSGDGTETISE GGSDDYTYTV YRDGTIKIEG LTATTFEEDG VAAGNHEYCV 900
EVKYTAGVSP KVKCDVTVEG SNEFAPVQNL TGSAGVQKVT LKWDAPNGTP NPNPNPNPNP 960
NPGTTTTSES FENGIPASWK TIDADGDGHG WKPGNAPGIA GYNSNGCVYS ESFGLGGIGV 1020
LTPDNYLITP ALDLPNGGKL TFWVCAQDAN YASEHYAVYA SSTGNDASNF TNALLEETIT 1080
AKGVRSPETAI GRIQGTWRQ KTVDLPGATK YVAFRHFQST DMFYIDLDEV EIKANGKRAD 1140
10 FTETFESSSTH GEAPAEWTTI DADGDGQGWL CLSSQQLDWL TAHGGTNVVS SPSWNGMALN 1200
PDNYLISKDV TGATKVKYVY AVNDGFPGDH YAVMISKTGT NAGDFTVVFE ETPNGINKGG 1260
ARFGLSTEAD GAKPQSVWIE RTVDLPAGTK YVAFRHYNCS DLNYILLDDI QFTMGGSPTP 1320
TDYTYTVYRD GTRIKIEGLTE TTFEEDGVAT GNHEYCVEVK YTAGVSPKKC VNVTVNSTQF 1380
NPVKNLKAQP DGGDVVLKWE APSAKKTEGS REVKRIGDGL FVTIEPANDV RANEAQVVL 1440
15 ADNVWGDNTG YQFLLDADHN TFGSVIPATG PLFTGTASSD LYSANFEYLI PANADPVVTT 1500
QNIIVTGQGE VVIPGGVYDY CITNPEPASG KMWIAGDGGN QPARYDDFTF EAGKKYTFM 1560
RRAGMGDGT MEVEDDSPAS YTYTVYRDGT KIKEGLTETT YRDAGMSAQ S HEYCVEVKYT 1620
AGVSPKVCVD YIPDGVADVT AQKPYTLTVV GKTTITVTCQG EAMIYDMNGR RLAAGRNTVV 1680
YTAQGGYAV MVVVDGKSYV EKLAIK 1706
20 <212> Type : PRT
<211> Length : 1706
SequenceName : SEQ ID 176
SequenceDescription :
25 Sequence

<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :
MKRKPLFSAL VILSGFFGSV HPASAKQVPA PVDGERIIME LSEADVECTI KIEAEDGYAN 60
30 DIWADLNGNG KYDSGERLDS GEFRDVEFRQ TKAIVYGKMA KFLFRGSSAG DYGFATFIDIS 120
NCTGLTAFDC FANLLTELDEL SKANGLTFVN CGKNQTKLD LPANADIETL NCSKNKITS 180
NLSTYTKLKE LYVGDNGLTA LDLSANTLLE ELVYSNNEVT TINLSANTNL KSLYCINNKM 240
TGLDVAANKE LKILHCNNNQ LTALNLSANT KLTTLSEFFNN ELTNIDLSDN TALEWLF 300
NKLTKL DVSA NANLIALQCS NNQLTALDLS KTKPLTTLNC YSNRIKDTAM RALIESLPTI 360
35 TEGEGRFVPIY NDEGEGEEEN VCTTEHVEMA KAKNWKVLTS WGEPPFGITA LISIEGESEY 420
SVYAQDGLY LSGMEQGLPV QVYTVGGSM YSSVASGSAM EIQLPRGAAY VVRIGSHA 480
TAMP 484
<212> Type : PRT
<211> Length : 484
40 SequenceName : SEQ ID 177
SequenceDescription :
Sequence

45 <213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRAITLFAV LLMGWSVNAW SFACKTANGT AIPIGGGSAN VYVNLAPVVN VGQNLVVDLS 60
TQIFCHNDYP ETITDYVTLQ RGSAYGGVLS NFSGTVKYSG SSYPFFTSE TPRVVYNSRT 120
DKPWPVALYL TPVSSAGGVA IKAGSLIAVL ILRQTNVNS DDFQFVWNIY ANNDVVVPTG 180
50 GCDVSARDVT VTLDPYPGSV PIPLTVYCAK SQNLGYLISG TTADAGNSIF TNTASFSPAQ 240
GVGVQLTRNG TIIPANNTVS LGAVGTSAVS LGLTANYART GGQVTAGNVQ SIIGVTFVYQ 300
<212> Type : PRT
<211> Length : 300
55 SequenceName : SEQ ID 178
SequenceDescription :
Sequence

60 <213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MGIKQHNGNT KADRLAELKI RSPSIQLIK GAIGLNAIIF SPLLIAADTG SQYGTNITIN 60
DGDRIITGDTA DPGSNLYGVM TPAGNTPGNI NLGNDVTNV NDASGYAKGI IIQKNSSLT 120
ANRLTVDVVG QTSAGINLI GDYTHADLGT GSTIKSNDG IIIGHSSTLT ATQFTIENS 180
65 GIGLTINDYG TSVDLGSGSK IKTDGSTGVY IGGLNGNNAN GAARFTATDL TIDVQGSAM 240
GINVQNSV DLGTNSTIKT NGDNAHGLWS FGQVSANALT VDVGTGAAANG VEVGGTTTI 300
GADSHISSAQ GGGLVTSSSD ATINFSGTAA QRNSIFSGGS YGASAQTATA VINMQNTDIT 360

VDRNGSLALG LWALSGGRIT GDSLAIITGAA GARGIYAMTN SQIDLTSDLV IDMSTPDQMA 420
IATQHDDGYA ASRINASGRM LINGSVLSKG GLINLDMHPG SVWTGSSSLD NVNGGKLDVA 480
MNNSVWNVTS NSNLDLTLALS HSTVDFASHG STAGTFTTLN VENLSGNSTF IMRADVVGE 540
NGVNNRGDGL NISGSSAGNH VLAI RNQSGE ATTGNEVLTV VKTTDGAASF SASSQVELGG 600
5 YLYDVRKNGT NWELYASGTV PEPTNPPEPT PAPAQPPIVN PDPTPEPAPT PKPTTTADAG 660
GNYLNVGYYL NYVENRTLMQ RMGDLRNQSK DGNIWLRSYG GSLSDFASGK LSGFDMGYSG 720
IQFGGDKRLS DVMPLYVGLY IDSTHASPDY SGGDGTARSD YMGMYASYMA QNGFYSDLVI 780
KASRQKNSFH VLDSQNNGVN ANGTANGMSI SLEAGQRFNL SPTGYGFYIE PQTQLTYSHQ 840
NEMAMKASNG LNIHLNHYES LLGRASMILG YDITAGNSQL NVYVKTGAIR EFSGDTEYLL 900
10 NDSREKYSFK GNGWNNNGGV SAQYNKQHTF YLEADYTQGN LFDQKQVNGG YRFSF 955

<212> Type : PRT
<211> Length : 955
SequenceName : SEQ ID 179
15 SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
20 <400> PreSequenceString :
MSKFVKTAIA AAMVMGVFTS TATIAAGNNG TARFYGTIED SVCSIVPDDH KLEVDMGDIG 60
AEKLNKNGTT TPKSFQIRLQ DCVFDTQETM TTTFTGTVSS ANSGNYTIF NTDTGAAFN 120
VSLAIGDSL GTSYKSGMGID QKIVKDTSTN KKGAKQTLNF NAWLVGAADA PDLGNFEANT 180
TFQITYL 187

25 <212> Type : PRT
<211> Length : 187
SequenceName : SEQ ID 180
SequenceDescription :

30 Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
35 MKIKTLAIVV LSALSLSAA ALADTTTVNG GTIHFKEGVV NAACAVDAGS VDQTVQLGQV 60
RTASLKQAGA TSSAVGFNIQ LNDCTTTVAT KAAVAFLGTA IDATRTDVL LQSSAAGSAT 120
NVGVQILDRT GNALTLDGAT FSAQTTLNNG TNTIPFQARY YAIGETPGA ANADATFKVQ 180
YQ 182

40 <212> Type : PRT
<211> Length : 182
SequenceName : SEQ ID 181
SequenceDescription :

Sequence

45 <213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MASISLGVG SGLDLSSILD SLTAAQKATL TPISNQSSF TAKLSAYGTL KSALTTFQTA 60
NTALSADLF SATSTTSST AFSATTAGNA IAGKYTISVT HLAQAQTLTT RTTRDDTKTA 120
IATSDSKLTI QQGDDKDPIT IDISAANSSL SGIRDAINNA KAGVSASIN VNGEYRLSV 180
50 TSNDTGLDNA MTLVSVGDDA LQSFMGYDAS ASSNGMEVSV AAQNAQLTVN NVAIENSNT 240
ISDALENITL NLNDVTTGNQ TLITITQDTSK VQTAIKDWNV AYNSLIDTFS SLTKYTAVDA 300
GADSQSSSNG ALLGDSTLRT IQTQLKSMLS NTVSSSSYKT LAQIGITTD P SDGKLELDAD 360
KLTAALKKDA SGVGALIVGD GKKTGITTTI GSNLTSWLST TGIKKAATDG VSKTLNKLTK 420
DYNAAASDRID AQVARYKEQF TQLDVLMTSL NSTSSYLTTQ FENNSNSK 468

55 <212> Type : PRT
<211> Length : 468
SequenceName : SEQ ID 182
SequenceDescription :

60 Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
65 MEGKADNVVL ENGGRLDVLT GHTATNTRVD DGGTLDVRNG GTATTVSMGN GGVLLADSGA 60
AVSGTRSDGK AFSIGGGQAD ALMLEKGGSSF TLNAGDTATD TTVNGGLFTA RGGTLAGTTT 120
LNNGAILTSL GKTVMNDTLT IREGDALLQG GALTNGSVE KSGSGTLTVS NTTLTQKAVN 180
LNEGTLTLND STVTDDVIAQ RGTALKLTGS TVLNGAIDPT NVTLASGATW NIPDNATVQS 240

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VVDLDSHAGQ IHFTSTRGK FVPATLKVKLN LNGQNGTISL RVRPDMQNN ADRLVIDGGR      300
ATGKTILNLV NAGNSASGLA TSGKGIQVVE AINGATTEEG AFIQGNKLQA GAFNYSLNRD      360
SDESWYLRSE NAYRAEVPLY ASMLTQAMDY DRILAGSRSH QTGVSGENNS VRLSIQGGHL      420
GHDNNGGIAR GATPESGSGY GFVRLEGDLI RTEVAGMSVT AGVYGAAGHS SVDVKDDGDS      480
5  RAGTVRDDAG SLGGYLNLIH NASGLWADIV AQGTRHSMKA SSDNNDFRVR GWGWLGSLET      540
GLPFSITDNL MLEPQLQYTW QGLSLDDGQD NASYVKFGHG SAQHVRAGFR LGSHHDMNFG      600
KGTSSRDTLR GSAKHSVREL PVNWWVQPSV IRTFSSRGDM SMGTAAAGSN MTFSPSQNGT      660
SLDLQAGLEA RVRENITLGV QASYAHSING SSAEGYNSQA TLNVTF                      706
<212> Type : PRT
10 <211> Length : 706
    SequenceName : SEQ ID 183
    SequenceDescription :

Sequence
-----
15 <213> OrganismName : Shigella flexneri 2a str. 2457T
    <400> PreSequenceString :
MAFSQAVSGL NAAATNLDDVI GNNIANSATY GFKSGTASFA DMFAGSKVGL GVKVAGITQD      60
FTDGTITNTG RGLDVAISQN GFFRLVDSNG SVFYSRNGQF KLDENRNLLN TQGLQLTGYP      120
20 VTGTPPTIQG GANPTNISIP NTLMAAKTTT TASMQINLNS SDPLPTVTPF SASNADSYNK      180
KGSVTVFDSQ GNAHMSVYF VKTGDNNWQV YTQDSSDPNS IAKTATTLEF NANGTLVDGA      240
MANNIATGAI NGAEPATFSL SFLNSMQQNT GANNIVATTQ NGYKPGDLVS YQINDDGTVV      300
GNNSNEQTQL LGQIVLANFA NNEGLASEGD NVWSATQSSG VALLGTAGTG NFGTLTNGAL      360
EASNVDSKE LVNMIVAQRN YKSNAQTIKT QDQILNTRVN LR                      402
25 <212> Type : PRT
    <211> Length : 402
    SequenceName : SEQ ID 184
    SequenceDescription :

Sequence
-----
30 <213> OrganismName : Shigella flexneri 2a str. 2457T
    <400> PreSequenceString :
MKLVHMASGL AVAIALACA DKSADIQTPA PAANTSISAT QQPAIQPNV SGTVWIRQKV      60
35 ALPPDAVLTV TLDASLADA PSKVLAKAV RTEGKQSPFS FVLFPNPADV QPNARILLSA      120
AITVNDKLVF ITDTVQPVIN QGGTKADLTL VPVQQTAVPV QASGGATTTV PSTSPTQVNP      180
SSAVPAPTQY                      190
    <212> Type : PRT
    <211> Length : 190
    SequenceName : SEQ ID 185
    SequenceDescription :

Sequence
-----
45 <213> OrganismName : Shigella flexneri 2a str. 2457T
    <400> PreSequenceString :
MIIKSGGRW QLSLLASVVI SAFFLNTAYA WQGEYIVDTQ PGHSTERYTW DSDHQPDYND      60
ILSQRIQSSQ RALGLEVNLA EETPVDVTSS MSMGWNFPY EQVTGTPVAA LHYDGTTSMT      120
YNEFGDSTTT LTDPLWHASV SSLGWRVDSR LGDLRPWAI SYNQQFGENI WKAQSGLSRM      180
50 TATNQGNWL DVTVGADMLL NQNIAYAAL TQAENTTNNS DYLYTMGVSA RF          232
    <212> Type : PRT
    <211> Length : 232
    SequenceName : SEQ ID 186
    SequenceDescription :

Sequence
-----
60 <213> OrganismName : Shigella flexneri 2a str. 2457T
    <400> PreSequenceString :
MKWCKRGYVL AAMLALASAT IQAADVTITV NGKVVAKPCT VSTTNATVDL GDLYSFSLMS      60
AGAASAWHDV ALELTNCPVG TSRVTASFSG AADSTGYIK QGTAQNIQLE LQDDSGNTLN      120
TGATKTQVD DSSQSAHFPL QVRALTVNGG ATQGTIQAVI SITYTYS                      167
    <212> Type : PRT
65 <211> Length : 167
    SequenceName : SEQ ID 187
    SequenceDescription :

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Sequence

5 <213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRAPLITGL LLISTSCAYA SSGGCGADST SGATNYSSVV DDVTVNQTDN VTGREFTSAT 60
LSSSTNWQYAC SCSAGKAVKL VYMVSPVLTG TGHQTGYVKL NDSLDIKTTL QANDIPGLTT 120
DQVVSVNTRF TQIKSSTVYS AATQTGVCQG DTSRYGPVNI GANTTFTLYV TKPFLGSMTI 180
PKTDIAVIK AWVDGMSGPS TGDHDLVVKL SIQGNLTAPQ SCKINQGDVI KVNFGFINGQ 240
10 KFTTRNAMPD GFTPVDFDIT YDCGDTSKIK NSLQMRIDGT TGVVDQYNLV ARRRSSDNVP 300
DVGIRIENLG GGVANIPFQN GILPVDPSGH GTVNMRAWPV NLVGGELETG KFQGTATITV 360
MVR 363
<212> Type : PRT
<211> Length : 363
15 SequenceName : SEQ ID 188
SequenceDescription :

Sequence

20 <213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MQKNAAHTYA ISSLLVLSLT GCAWIPSTPL VQGATSAQPV PGPTPVANGS IFQSAQPINY 60
GYQLPFEDRR PRNIGDTLTI VLQENVASAK SSSANASRDG KTNFGFDTVP RYLQGLFGNA 120
RADVEASGGN TFNGKGGANA SNTFSGTLTV TVDQVLVNGN LHVVGKQIA INQGTFFIRF 180
25 SGVVNPRTIS GSNTVPSTQV ADARIEYVGN GYINEAQNMG WLQRFFLNLS PM 232
<212> Type : PRT
<211> Length : 232
SequenceName : SEQ ID 189
30 SequenceDescription :

Sequence

35 <213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRHLNTCYR LVWNHITGAF VVASELARAQ GKRGGVAVAL SLAAVTSPLV LAADIVVHPG 60
ETVNGGTLVN HDNQFVSGTA DGVTVSTGLE LGPDSDENTG GQWIKAGGTG RNTTVTANGR 120
QIVQAGGTAS DTVIRDGGGQ SLNGLAVNTT LDNRGEQWVH GGGKAAGTII NQDGYQTIKH 180
GGLATGTIIV TGAEGGPESE NVSSGQMVG G TAESTTINKN GRQVIWSSGM ARDTLIYAGG 240
40 DQTVHGEAHN TRLEGGNQYV HNGGTATETL INRDGWQVIK EGGTAAHTTI NQKESCR 297
<212> Type : PRT
<211> Length : 297
SequenceName : SEQ ID 190
45 SequenceDescription :

Sequence

50 <213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MMMKTIKHLL CCAIAASALI STGVHAASWK DALSSAASEL GNQNSTTQEG GWSLASLTNL 60
LSSGNQALSA DNMNNAAGIL QYCAKQKLAS VTDAENIKNQ VLEKLGLNSE EQKEDTNYLD 120
GIQGLLKTGD GQQLNLDNIG TTPLAEKVKT KACDLVLKQG LNFIS 165
<212> Type : PRT
55 <211> Length : 165
SequenceName : SEQ ID 191
SequenceDescription :

Sequence

60 <213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MFKGQKTLAA LAVSLLFTAP VYAADEGSGE IHFKGEVIEA PCEIHQDDID KEVELGQVTT 60
SHINQSHHSD AVAVDLLLVN CDLENSNGS GKGISKVAVT FDSSAKTTGA DPILNNTSTG 120
65 EATGVGVRLM NKDQSNIVLG TATPDIDLAP TSSEQTLNFF AWMEQIDQAT PVTPGAUTAN 180
ATYVLDYK 188
<212> Type : PRT

<211> Length : 188
SequenceName : SEQ ID 192
SequenceDescription :

5 Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MSAGSPKFTV RRIAALSLVS LWLAGCSDTS NPPAPVSSVN GNAPANTNSG MLITPPPKMG 60
TTSTAQQPQI QPVQQPQIQ TQQPQIQPVQ PVAQQPVQME NGRIVYNRQY GNIPKGSYSG 120
10 STYTVKKGDT LFYIAWITGN DFRDLAQRNN IQAPYALNVG QTLQVGNASG TPITGGNAIT 180
QADAAEQGVV IKPAQNSTVA VASQPTITYS ESSGGEQSANK MLPNNKPTAT TVTAPVTVPT 240
ASTTEPTVSS TSTSTPISTW RWPTEGKVIE TFGASEGGNK GIDIAGSKGQ AIIATADGRV 300
VYAGNALRGY GNLIILIKHND DYLSAYAHND TMLVREQQEV KAGQKIATMG STGTSSTRLH 360
15 FEIRYKKGXV NPLRYLPQR 379

<212> Type : PRT
<211> Length : 379
SequenceName : SEQ ID 193
SequenceDescription :

20 Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
25 MIKFLSALIL LLVTTAAQAE RIRDLSVQV VRQNSLIGYG LVVGLDGTGD QTTQTPFTTQ 60
TLNNMLSQLG ITVPTGTNMQ LKNVAAMVT ASLPPFGRQG QTIDVVVSSM GNAKSLRGGT 120
LLMTPLKGVD SQVYALAQGN ILVGGAGASA GGSSVQVNQL NGGRITNGAV IERELPSQFG 180
VGNTLNLQLN DEDFSMAQQI ADTINRVRGY GSATALDART IQVRVPSGNS SQVRFLADIQ 240
NMQVNVTPQD AKVVINSRTG SVVMNREVTI DSCAVAQGNL SVTVNRQANV SQPDTPFGGG 300
30 QTVVTPQTQI DLRQSGGSLQ SVRSSASLNN VVRALNALGA TPMDLMSILQ SMQSAGCLRA 360
KLEII 365

<212> Type : PRT
<211> Length : 365
SequenceName : SEQ ID 194
SequenceDescription :

35 Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
40 MKRSIIAAAV FSSFFMSAGV FAADVDTGTL TIKGNIAESP CKFEAGGDSV SINMPTVPTT 60
VFEKGAKYST YDDAVGVTSS MLKISCPKEV AGVKLSLITN DKITGNDKAI ASSNDFVGDN 120
SDVLDVSAPP NIESYKTAEG QYAIPFKAKY LKLTDNSVQS GDVLSLVMR VAQD 174

<212> Type : PRT
<211> Length : 174
SequenceName : SEQ ID 195
SequenceDescription :

50 Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MAVQKNVIKG ILAGTFALML SGCVTVPDAI KGSSTTPQQD LVRVMSAPQL YVGQEARFGG 60
55 KVVAVQNQQG KTRLEIATVP LDGARGPTLG EPSRGRIYAD VNGFLDPVDF RGQLVTVVGP 120
ITGAVDGKIG NTPYKFMVMQ VTGYKRWHLT QQVIMPPQPI DPWFYGGRGW PYGYGGWGWY 180
NPGPARVQTV VTE 193

<212> Type : PRT
<211> Length : 193
SequenceName : SEQ ID 196
SequenceDescription :

60 Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MRNKPFYLLC AFLWLAVSRV LAADSTITIR GYVRDNGCSV AAESTNFTVD LMENAAKQFN 60

NIGATTPVVP FRILLSPCGN AVSAVKVGFT GVADSHNANL LALENTVSAA AGLGIQLLNE 120
QQNQIPLNAP SSAISWTTLT PGKPNTLNFY ARLMATQVPV TAGHINATAT FTLEYQ 176

<212> Type : PRT
5 <211> Length : 176
SequenceName : SEQ ID 197
SequenceDescription :

Sequence
10 -----
<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKLTVAALA VTLLSGSAF AHEAGEFFMR AGSATVRPTE GAGGTLGSLG GFSVTNNTQL 60
GLTFTYMATD NIGVELLAAT FFRHKIGTRA TGDIA TVHHL PPTLMAQWYF GDASSKFRPY 120
15 VGAGINYTTF PDNGFNDHGK EAGLSDSLK DSWGAAGQVG VDYLINRDWL VNMSVWYMDI 180
DTTANYKLGG AQQHDSVRLD PWVFMFSAGY RF 212

<212> Type : PRT
<211> Length : 212
SequenceName : SEQ ID 198
20 SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
25 <400> PreSequenceString :
MFFKRGKILS AGRLNKKS LG IVMFLSVGLL LAGCSGSKSS DTGTYSGSVY TVKRGDTLYR 60
ISRTTGTSTVK ELARLNGISP PYTIEVGQKL KLGAKSSSS TRKSTAKSTT KTASVTPSSA 120
VPKSSWPPVG QRCWLWPTTG KVIMPYSTAD GGNKGIDISA PRGTPPIYAAG AGKV VYVGNQ 180
LRGYGNLIMI KHS EYITAY AHNDTMLVNN GQSVKAGQKI ATMGSTDAAS VRLHFQIRYR 240
30 ATAIDPLRYL PPQGS KPKC 259

<212> Type : PRT
<211> Length : 259
SequenceName : SEQ ID 199
SequenceDescription :

35 Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
40 MAQVINTNSL SLITQNNINK NQSALSSSIE RLSSGLRINS AKDDAAGQAI ANRFTSNIKG 60
LTQAARNAND GISVAQTTEG ALSEINNMLQ RIRELTVQAS TG TNSDSLD SIQDEIKSRL 120
DEIDRVSGQT QFNGVNV LAK DGSMKIQVGA NDGQTITIDL KKIDSDTLGL NGFN VNGGGA 180
VANTAASKAD LVAANATVVG NKYTVSAGYD AAKASDLLAG VSDGDTVQAT INNGFGTAAS 240
ATNYKYDSAS KSYSFDTT TA SAADVQKYL T PGVGD TAKGT ITIDGSAQDV QISSDGKITA 300
45 SNGDKLYIDT TGR LTKNGSG ASLTEASLST LAANNTKATT IDIGGTSISF TGNSTTPDTI 360
TYSVTGAKVD QAAFDKAVST SGNNVDFTTA GYSVNGTTGA VTKGVDSVYV DNNEALTTSD 420
TVDFYLQDDG SVTNGSGKAV YKDADGKLTT DAETKAATTA DPLKALDEAI SSIDKFRSSL 480
GAVQNR LDSA VTNLNNTT TN LSEAQSRIQD ADYATEVSNM SKAQIIQQAG NSVLAKANQV 540
PQQVLSLLQG 550

50 <212> Type : PRT
<211> Length : 550
SequenceName : SEQ ID 200
SequenceDescription :

55 Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
60 MKKIACLSAL AAVLAFTAGT SVAATSTVTG GYAQSDAQGQ MNKMGGFNLK YRYEEDNSPL 60
GVIGSFYTE KSR TASSGDY NKNQYYGITA GPAYRINDWA SIYGVVGVGY GK FQTTEYP T 120
YKHDTS DYGF SYGAGLQFNP MENVALDFS Y EQSRIRSV DV GTWIAGVGYR F 171

<212> Type : PRT
<211> Length : 171
65 SequenceName : SEQ ID 201
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
5 MKRNIIGGAF TLASLMLAGH ALAEDGVVNF VGEIVDTTCE VTSDTADQIV PLGKVSNAF 60
SGVGLASPQ KFSIKLENC P ATYTQAAVRF DGTEAPGGDG DLKVGTPPLTA GNP GDFTGTG 120
QAIAATGVGI RIFNQSDNSQ VKLYNDSAYT AIDAEGKAEM KFIARYVATN ATVTAGTANA 180
DSQFTVEYKK 190
<212> Type : PRT
10 <211> Length : 190
SequenceName : SEQ ID 202
SequenceDescription :

Sequence

15 <213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKSTLALVV MGIVASASVQ AAEIYNK DGN KLDVYGK VKA MHYMSDNASK DGDQSYIRFG 60
FKGETQINDQ LTGYGRWEAE FAGNKAESDT AQKQTRLAFA GLKYKDLGSF DYGRNLGALY 120
20 DVEAWTDMFP EFGGDSSAQ T DNFMTKRASG LATYRNTDFF GVIDGLNLTL QYQGKNENRD 180
VKKQNGDGFQ TSLTYDFGGS DFAISGAYTN SDRTNEQNLQ SRGTGKRAEA WATGLKYDAN 240
NIYLATFYSE TRKMTPI TGG FANKTQNF EA VAQYQDFDGL RPSLGYVLSK GKDIEGIGDE 300
DLVNYIDVGA TYFFNKNMSA FVDYKINQLD SDNKLININD DTVAVGMTYQ F 351
<212> Type : PRT
<211> Length : 351
SequenceName : SEQ ID 203
SequenceDescription :

30 Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MRKQWL GICI AAGMLA ACTS DDGQQQT VSV PQPAVCNGPI VEISGADPRF EPLNATANQD 60
35 YQRDGKSYKI VQDPSRFSQA GLAAIYDAEP GSNLTASGEA FDP TKLTAAH PTLPIPSYAR 120
ITNLANGEMI VVRINDRGPY GNDRVISLSR AAADRLNTSN NTKVRIDPII VAQDGSLSGP 180
GMACTTVAQK TYALPAPPDL SGGAGTSSVS GPQGDILPVS NSTLKS EDP T GAPVTSSGFL 240
GAPTTLAPGV LEGSEPTPAP QPVVTASSTT PATSPAMVTP QAASQSASGN FMVQVGAVSD 300
QARAQQYQQQ LGQKFGVPGR VTQNGAVWRI QLGPFAKAE ASTLQQLQT EAQLQS FITT 360
40 AQ 362
<212> Type : PRT
<211> Length : 362
SequenceName : SEQ ID 204
SequenceDescription :

45 Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
50 MKKKTIYQCV ILFFSLLNIH VGMAGPEQVS MHIYGNVVDQ GCDVATKSAL QNIHIGDFNI 60
SDFQAANTVS TAADLNIDIT GCAAGITGAD VLFSGEADTL APTLLKLTDT GGSGGMATGI 120
AVQILDAQSQ QEIPLNQVQP LTPLKAGDNT LKYQLRYKST KAGATGGNAT AVLYFDLVYQ 180
<212> Type : PRT
55 <211> Length : 180
SequenceName : SEQ ID 205
SequenceDescription :

60 Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKNKLLFMML TILGAPGIAA AAGYDLANSE YNFAVNELSK SSFNQAAIIG QAGTNNSAQL 60
RQGGSKLLAV VAQEGSSNRA KIDQTGDYNL AYIDQAGSAN DASISQ GAYG NTAMITQKGS 120
65 GNKANITQYG TQKTAVVVQR QSQMAIRVTQ R 151
<212> Type : PRT
<211> Length : 151

SequenceName : SEQ ID 206
SequenceDescription :

Sequence

5 <213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MMKFKKCLLP VAMLASFTLA GCQSNADDHA ADVYQTDQLN TKQETKTVNI ISILPAKVAV 60
GGVVVGRVAD ITLDPKTYLP RVLEIEQRY NHIPDTSSLS IRTSGLLGEQ YLALNVGFED 120
10 EGVSLTYKEG TKVYTSTQEG KECQFTTGLA VVITTYNET RIQPNTKCPE KS 172

<212> Type : PRT
<211> Length : 172
SequenceName : SEQ ID 207
SequenceDescription :

Sequence

20 <213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MQTKKNEIIV GIFLLAALLA ALFVCLKAAN VTSIRTESTY TLYATFDNIG GLKARSPVSI 60
GGVVVGRVAD ITLDPKTYLP RVLEIEQRY NHIPDTSSLS IRTSGLLGEQ YLALNVGFED 120
PELGTAILKD GDTIQDTKSA MVLEDLIGQF LYGSKGDDNK NSGDAPAAAP GNNETTEPVG 180
TTK 183

25 <212> Type : PRT
<211> Length : 183
SequenceName : SEQ ID 208
SequenceDescription :

30 Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
35 MAPLAFSAQS LAESLTVEQR LELLEKALRE TQSELKKYKD EEKKKYTPAT VNRSVSTNDQ 60
GYAANPFPTS SAAKPDVAVL KNEEKNASET GSIYSSMTLK DFSKFVKDEI GFSYNGYIRS 120
GWGTASHGSP KSWAIGSLGR FGNEYSGWFD LQLKQRYNE NGKRVDAVVM IDGNVGGQYS 180
TGWFGDNAGG ENFMQFSDMY VTTKGFLPFA PEADFWVGKH GAPKIEIQML DWKTQRTDAA 240
AGVGLENWKV GPGKIDIALV REDVDDYDRS LQNKQQINTH TIDLRYKDIP LWDKATLMVS 300
GRYVTANESA SEKDNQDNNG YYDWKDTWMF GTSLTQKFDK GGFNEFSFLV ANNSIARNFG 360
40 RYAGASPFTT FNGRYYGDHT GGTAVRLTSQ GEAYIGDHFI VANAIIVYSFG NNIYSYETGA 420
HSDFESIRAV VRPAYIWDQY NQTGVELGYF TQQNKDANSN KFNESGYKTT LFHTFKVNTS 480
MLTSRLERIF YATYIKALEN ELDGFTFEDN KDAQFAVGAQ AEIWW 525

<212> Type : PRT
<211> Length : 525
45 SequenceName : SEQ ID 209
SequenceDescription :

Sequence

50 <213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKRILSAVL VSGVTLSST TLSAVKADDF DAQIASQDSK INNLTAAQQA AQAQVNTIQG 60
QVSALQTQQA ELQAENQRLE AQSATLGQQI QTLSSKIVAR NESLKQQARS AQKSNAATSY 120
INAIINSKSV SDAINRVSAI REVVSANEKM LQQEQQDKAA VEQKQQENQA AINTVAANQE 180
55 TIAQNTNALN TQQAQLEAAQ LNLQAELETTA QDQKATLVAQ KAAAEAAARQ AAAAQAAAEA 240
KAAAEAKALQ EQAAQAQAAA NNNTQATDVS DQQAADANT QAAQTGDSTE QSAAQAVNNS 300
DQESTTATEA QPSASSASTA AVAANTSSAN TYPAGQCTWG VKSLAPWVGN YWNGGGQWAA 360
SAAAAGYRVG STPSAGAVAV WNDGGYGHVA YVTGVQGGQI QVQEANYAGN QSIGNYRGWF 420
NPGSVSYIYP N 431

60 <212> Type : PRT
<211> Length : 431
SequenceName : SEQ ID 210
SequenceDescription :

65 Sequence

<213> OrganismName : Streptococcus mutans UA159

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<400> PreSequenceString :
MKVKKTYGFR KSKISKTLCG AVLGTVAAVS VAGQKVFAD E TTTSDVDTK VVGTTQGNPA      60
TNLPEAQGSA SKEAEQSQNQ AGETNGSIPV EVPKTDLDQA AKDAKSAGVN VVQDADVNKG      120
TVKTAEEAVQ KTEIKEDYT KOAEDIKKT DQYKSDVA AH EAEVAKIKAK NQATKEQY EK      180
5 DMAAHKAEVE RINAANAASK TAYEAKLAQY QADLA AVQKT NAANQAAYQK ALAAYQAE LK      240
RVQEANA AAK AAYDTAVAAN NAKNTEIAAA NEETRKNAT AKA EYETKLA QYQAE LKRVQ      300
EANAANEADY QAKLTAYQTE LARVQKANAD AKAAYEAAVA ANNAKNAALT AENTA IKQRN      360
ENAKATYEAA LKQYEADLAA VKKANAANEA DYQAKLTAYQ TELARVQKAN ADAKAA YEAA      420
VAANNAANAA LTAENTA IKK RNADAKADYE AKLAKYQADL AKYQKDLADY PVK LKAYEDE      480
10 QASIKAAALAE LEKHKNEDGN LTPESAQNLV YDLEPNANLS LT TDGKFLKA SAVDDAFSKS      540
TSKAKYDQKI LQLDDLDITN LEQSN DVASS MEL YGNFGDK AGWSTTVSNN SQVKWGSVLL      600
ERGQSATATY TNLQNSYYNG KKISKIVYKY TVDPKSKFQG QKVWLGI FTD PTLGVFASAY      660
TGQVEKNTSI FIKNEFTFYD EDGKPIFN DN ALLSVASLNR ENNSIEMAKD YTGK FVKISG      720
SSIGKNGMI YATDTLNF RQ GQGGARWTMY TRASEPGSGW DSSDAPNSWY GAGAIRMSGP      780
15 NNSVTLGAIS STLVPADPT MAIETGKKPN IWYSLNGKIR AVNVPKVTKE KPTPPVKPTA      840
PTKPTYETEK PLKPAPVAPN YEKEPTPPTR TPDQAE PNKP TPPTYETEK PLEPAPVEPSY      900
BAEPTPPTRT PDQAE PNKP PPTYETEK PL EPAPVEPSY AEPTPPTPT DQPEPNKPVE      960
PTYEPIPTPP TDPVYQDLPT PPSVPTVHFH YFKLAVQPQV NKEIRNNNDI NIDRTLVAQK      1020
SVVVKQLKTA DLPAGRDETT SFVLVDPLPS GYQFNPEATK AASPGFDV TY DNATNTVTFK      1080
20 ATAATLATFN ADLTKSVATI YPTVVGQVLN DGATYKNNFT LTVNDAYGIK SNVVRVTT PG      1140
KPNDPDNPNN NYTKPTKVNK NENGVIDGK TVLAGSTNY Y ELTWDL DQYK NDRSSADTIQ      1200
KGFYYVDDYP EEALELRQDL VKITDANGNE VTGSVDNYT NLEAAPQEIR DVL SKAGIRP      1260
KGAFQIFRAD NPREFYDTYV KTGIDLKIVS PMVVKQMGQ TGGSYENQAY QIDFGNGYAS      1320
NIIINNVPKI NPKKDVT LTL DPADTNNDVG QTIPLNTVFN YRLIGGIIPA DHSEELFEYN      1380
25 FYDDYDQTDG HVTGQYK VFA KVDITFKDGS IIKSGAELTY YTTAEVD TAK GAITIKFKEA      1440
FLRSVSIDSA FQAESYIQMK RIAVGTFENT YINTVNGVTY SSNTVKTTTP EDPTDPTDPQ      1500
DPSSPRTSTV INYKPQSTAY QPSSVQETLP NTGVTNNAYM PLLGIIGLVT SFSLLGLKAK      1560
KD                                                                    1562

<212> Type : PRT
30 <211> Length : 1562
    SequenceName : SEQ ID 211
    SequenceDescription :

Sequence
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35 <213> OrganismName : Streptococcus mutans UA159
    <400> PreSequenceString :
MLTELKAVLK KPMLWITMVG VALVPALYNI IFLSSMWDPY GKVSDLPVAV VNKDKTATYE      60
GKKMTIGKDM TDMMVRN KSL DYHFVDSEKA QKGLEKGDY Y MIITLPEDLS QNAASVLTDE      120
40 PKKLTIPYQT SKGHSFVASK MSETAAKTLK ESVSKNITSS YTKSLFKNMS TLKTGLGSAA      180
NASQKIATGS KQLANGSQVM TDNLNL LNSNS SQSFAQGTNT LYSGLTAYTG GVGQLSAGLN      240
NLNNGLTAYT NGVGQLANGS SQLSNQSQKL LGGVAQLANG SASIQQLVNA SSQLNQGLIK      300
LSTATGLSEE VQQQFSSLIN QLGTNLQSIQ NYSDNGTATT ANSPDLSTYL SAITTAQAI      360
VNSGNTSQQT TTNQSNALAA VQATGAYQRL SAEDQSEIAA ALANTGSSTT TTGADANAVS      420
45 QAQAILNNVQ SIQSALSTLQ TTTANTPTSP SASLTQIKNT ANSVLP SAAT SLTTLSSGLT      480
QAKTALDSQV VPVSTALANG TAQLGSTFST GANSIMTGVG QYTNAVDILN AGANTLAAKN      540
NQLTDGTSQL VNGANQLNSN SGQLTKGTAQ LANGANQIET GAGKLAAGGE SLTAGLTTLS      600
SGSGELSKAL STAKNKL SLV AVDNDNAKTL SSPVTIKHTD KDNVKTNGVG MAPYMM SAAL      660
MVMAISTNTI FRVALSGKQA KTLREWIDQK LAVNGLIAVT GAILLYFGVH IIGLSANFEL      720
50 KTLGLLIILTS ITFMVLVTTL VTWHDKFSGF AALILL LLLQL GSSAGTYPLA VTDKFFQVVN      780
PYLPMSYSVS GLRETISMAG TIGNQLLALS LFFLTFAALG LLIARRRIRS VKVA          834

<212> Type : PRT
<211> Length : 834
55 SequenceName : SEQ ID 212
    SequenceDescription :

Sequence
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60 <213> OrganismName : Streptococcus mutans UA159
    <400> PreSequenceString :
MVSQKNKSKK GQSKTFTLIS NRINLLFFLI VALFTVLLLR LAQMQLYDAK FYKSKLTEST      60
TYTIKTSSPR GQIYDAKGVA L VENEVKEVV AFTRSNTMTA KDIKANAKKL ADMVTLTESK      120
VTKRQKDYD LADPKNYQKI VKKLPNNKKY DNFQNNLTES KTYANAVKAV PNSAIDYSED      180
65 EKKI IHIFSQ MNATSVFNTA SLTTGDLTAE QIAVLATSKS DLKGISVKTD WERKTDKNSI      240
TSIIGKVSSQ KTGLPAEEAN NYVKKGYSLN DRVGTSYLEK QYENDLQGSR TVQAIKVNKE      300
GKIISDKTTA KGTKGKNLKL TLDLEFQKGV EQILNQYFNS ELASGNTKYS EGVYAVVLNP      360

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NTGAVLSMAG LEHDLKTGEV SSNALGAVTE VFTPGSVVKG ATLTAGWENG VLSGNQVLND 420
QPIQFAGSSP INSWFTNGST PLTASQSLEY SSNTYMQVLA LKLMGQDYHS GMTLSTDGYK 480
EAMEKLRATY AQYGLGVSTG IDLPGESKGY TPEHYDPSNV LTESFGQFDN YTAMQLAQYA 540
AAVANGGKRI APHLVEGIYD NNKTGGLGNL VQSIDTKVLN NVSISSDDMG I IKEGFYNV 600
5 NGGSYATGKT LAKGASVPIS AKTGTAAYV TGDDGKSVYT SNLNVVAYAP SSNPQIAVAV 660
VLPHETDLHG TTSHAIRTDI INLYQKMYPM NQ 692
<212> Type : PRT
<211> Length : 692
SequenceName : SEQ ID 213
10 SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
15 <400> PreSequenceString :
MTVLKYGLGI LLSAII LAII IGGLLFTTYV SSTPKLSEAK LKATNSSLVY DSNNNLIADL 60
GAEKRESISS DSIPMKLVNA VTSIEDHRFF KHRGVDIYRI IGAAWSNLLH KSTQGGSTLD 120
QQLIKLAYFS TKESDQTLKR KAQEVWLSLQ MEKKYTKEEI LTFYVNKVYM GNGNYGMRTA 180
AKSYYGKDLK DLSIAQLATL AGIPQAPTQY DPYAQPKAAT SRRNTVLSQM YKHKKITKRE 240
20 YDAAVATPIS DGLQELKRSS SYPKYMDNYL KQVISEVKKR TGQDIFSAGM KVTYTNVNADA 300
QQYLWNIYNT DEYIAYPDDN FQVASTVMDV TNGKVIAQLG GRHODTNVSF GTNQAVALTDR 360
DWGSTMKPIS AYGPALSEEA FTTTAQMLND SVYYYPGTTT QVYDWDHRYN GWMTIQTAIQ 420
QSRNVPVAVRA IDAAGLD TAK GFLSGLGIDY PEMRYSNAIS SNTSSSEQKY GASSEKMAAA 480
YAAFSNGGT YEPQYVNKIE FKDGTSSETD AKGNRAMKET TAYMMTDMLK TVLTYGTGTE 540
25 AAIPGLYQAG KTGTSNYDDN ELVEMSEKLG INPYGLGTIA PDENFVGYP QYSMAVWTGY 600
KNRLMPVYGD SMKIAAQVYR TMMAYLSSSG NSDWTMPDGL YRSGGYLYLN GSSGNSRYG 660
AAPATSSSSS SSSSSDSNNN DQNNNQTTTEA SSDSSSSSSD ATTSSNP 707
<212> Type : PRT
<211> Length : 707
30 SequenceName : SEQ ID 214
SequenceDescription :

Sequence

35 <213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKSKTAKITL LSSSLAALAFG ATNVFADEAS TQLNSDTVAA PTADTQASEP AATEKEQSPV 60
VAVVESHTQG NTTTTTSQVT SKELEDAKAN ANQEGLEVTE TEAQKQPSVE AADADNKAQA 120
QTINTAVADY QKAKAEFPQK QEQYNKDFEK YQSDVKEYEA QKAAEQYK EYVAGLASGR 180
40 VEKAQGLVFI NEPEAKLSIE GVNQYLTKEA RQKHATEDIL QQYNTDNYTA SDFQTANPYD 240
PKEDTWFMMK VGDQISVTYD NIVNSKYNDK KISKVKINYT LNSSTNNEGS ALVNLFDHPT 300
KTIFIGAQTS NAGRNDKISV TMQIIFYDEN GNEIDLGN NAIMSLSSLNH WTTKYGDHVE 360
KVNLDGNEFV KIPGSSVDLH GNEIYSAKDN QYKANGATFN GDGADGWDAV NADGTTPRAAT 420
AYYGAGAMTY KGEPFTFTVG GNDQNLPTTI WFATNSAVAV PKDPGAKPTP PEKPELKKPT 480
45 VTWHKNLVE TKTEEVPPVT PPTTPDEPTP EKPKTPEDPQ SPVVAKSVSF RTARKGEMRV 540
RERDYQPTLP HAGAAKQNGL ATLGAISTAF AAATLIAARK KEN 583
<212> Type : PRT
<211> Length : 583
50 SequenceName : SEQ ID 215
SequenceDescription :

Sequence

55 <213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MEQKIFSKRK SKIAGLCGAI LTTTVVALAS GTVIEADETI EQPVAAETVS QADGDNPEQT 60
TSVQOETAPQ QTKTSQSSDA TVDSEESATS PSDEQTVSQN DSNSSSQIDQ TIADTNRSDS 120
DHISKTSAAAT TEDQEEKVNS AKAQTAAATN NQDTRYSAKD AYGNSTFNKT LTFEGKNANV 180
ADVTYNGVRD EYIVVNDPSA PYVPNANEIA KYLKEYLTEL RNINNIAIPV PSVDQVMQKY 240
60 AQDRANEEAN EKNGLDHDN LPIPNLTLTW AEDGHLDMDS SIQSKSQEGY TLASDKATAY 300
YIALNWFSYD FNIYDDPNDG LKSFHGAHSI LSDGGTGMGL GLASGQDNEK GMWYAQLEFG 360
GNDNEDNTND FSSLKNGKGE WVLYYKGSVP KFLPNTTFWY VKKGTSPDAA STPHNSDKPS 420
FQSSKDLDPN FKADNRFOEG KEASVHQAIP ATFKSHRDEV GNKDQNSLSA QLPDGTGVQKN 480
NQLALIALGT GLILLSGLLL SKRKSLK 507
65 <212> Type : PRT
<211> Length : 507
SequenceName : SEQ ID 216

SequenceDescription :

Sequence

5 <213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MTFEKQKHFS LRKLKFLVLS VAIIAFLFAV TKTAEADTV ITEQRQTSKI NASSQKVENQ 60
TSNQVEAKTD SANKDPQEK TGSVATDAPSM NSANNMSQSD KQNTVNEISS DSQQTKTDEQ 120
TDLFPQNSFKQ QSAHVKMTTE AEKTPSHSIN TFVNDGNGNW YYLGADGRNV TGSHTIGGKT 180
10 MYFAQDGKQV KGAFADSDG NKHYDRDSG EMWTRNFVND QGNWYYLNND GVPVGTGSITV 240
NGQSLYFNDS GSQVKGNFVE EDGSLRYDK NSGDLRLKTS RTINGVNYQF DNDGNARAID 300
KIEVVKTSVL VDSYEFGPSV SKIILEFNHK VTPAVVHAGA MVTTAGVQRK ILNSYVSNAS 360
GHVVYFDSSH YVLELDIPY DPNDSSRNAS PFIFDSAAFR NNWVNSYTVK VDNLQVQADG 420
SNSSQIISSE QDAINNRFPL TDRFSERGS YGNFNYYAYQ PEAAIGGEKN PLIVWLHGIG 480
15 EVGTIDINPL LASNVARLTE DPIQSHFTST GSGGQKGAYV LVPQSSIPWS QNQTASLMAL 540
IKAYVASHPD IDSRRYLAG VSNGGGMTLD MGVAYPNYFA ALVPPIAASYS NQLTDNQITA 600
AALKALKGQP MWLIHTRTDK TISADSSVLP FYKELLQAGA QNKWLSYYET NVGKHHSQVT 660
YNGHWSWIYF LNDQVTGTQN TDNAKNWSGL SGMVATNPTY GGDATATVNG RTYSNVFDWL 720
NGQRRR 726
20 <212> Type : PRT
<211> Length : 726
SequenceName : SEQ ID 217
SequenceDescription :

Sequence

25 <213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKIFIKKHQQ SILYYSLSFL LPSFIMFLVL FSKNIYWGS TITLASDGFH QYVIFDALFR 60
30 NILHGTDSL FYSFAGLGFN IFALTSYYLG SFLTPFTYFF NVKNMADAFY LFTLIKFGLI 120
GLSAFYSLGQ IYTKISKSLV LMLSTSYALM SFTSSQLELN NWLDVFI LLP LIMLGLQLRV 180
EKRGIFLYFL TLTCFLIQNY YFGFMTAIFL TLWFFTQVSW DIRNRMKRLS DFVLVSIFAT 240
LTSAFMLLPT FLDLKSHEV LTEQISLFSS DIWYDFFAK SLLGSYDTTK YGSIPTIYIG 300
LLPLIFAITE FVKSIIKQV KVAYFLLLAI IASFIQPL DLFWQGMHSP NMFLHRYSWA 360
35 FSLVIVIMAA ETLTRIKDIK LKNFYPAFTF LGVGLLATFL FKDYNNYLTQ VNFILTTIFL 420
VSYFIILFTF FNQLVSYKVI ISFTLIFTSE EIALNTFYQI EGIQTDWNP SREVYEDNVK 480
EIDNVVKKTK KDNLEFFRTE KQIPQTYNDG MKFNYSISQ FSSVKNNLSA QLLNSLGYYS 540
QGNHSTISYP NNTILMDSL FSIKYNINQN PHKFGFHLKQ KNNKLQLYKN FYSPLPLALMS 600
NHIYKDVKFD SYPLDNQKQF VNELTDLNLT LFKBIPIISS VGMQVLDNRV TINGSKGNKA 660
40 QVYTVKCPA NSQLYISLPN LTVNNKDNV FITNKHSTSS YIIDESYYLF NLGNYKKTQT 720
LIFKLSPKN KTVSYDLPHI YALDLTAYQK SIKQLKSQTV KTTTKKNKIF TTYVAKKRTS 780
LIYTLPPYDKG WFAKQNGKAI KISKAQNGLM KIDVSKGSGK IIMTFVPQGL YQGILLTCLG 840
IFLFVFPQLY YKKFNLK 857
45 <212> Type : PRT
<211> Length : 857
SequenceName : SEQ ID 218
SequenceDescription :

Sequence

50 <213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKLKHILRIG AVAFASILL TACGSKTSKK TVTLATVGT NPFSYEKKGK LTGYDIEVAK 60
EVFKASDKYD VKYQKTEWTS IFSGLDSDKY QIGANNISYT KERANKYLYS NPTASNPLVL 120
55 VVPKDSDIKS YNDIAGHSTQ VVQGNITVSM LQKFNKNHEN NQVKLNFTSE DLAHQIRNVS 180
DGKYDFKIFE KISAETIIE QGLDNLKVID LPSDQKPYVY FIFAQDQKDL QKFVNKRLKK 240
LYENGTLEKL SKKYLGGSYL PDKKDMK 267
60 <212> Type : PRT
<211> Length : 267
SequenceName : SEQ ID 219
SequenceDescription :

Sequence

65 <213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MRFLVFLIAF FAFYKFIET ERIDSNVAV NPDSLILKRF LKTNQLNGIM IVTGPDKAQ 60

VFSNQSKVDG SPVSIKDYFP LASLQKLITG VAIQQLIDKG KLSLNTPLSK YYPQIENSEN 120
ITIQNLLTHT SGLADRKEVP QQVLTQEQQ LDFSLTNYRV TYRKKWKYAN INYALLAGII 180
SQISGQNYAT YVRQHFLTAG KGWHFKKYYIQ IKDKSKLAAL SVMQDSTWD KLSKEVTSTF 240
GAGDYASRPV DYWKFMMAFI NDQFVPVSEY QRSKMKTSKS YYGGLYISQK MLHANGGGFD 300
5 TYSCFAYSNP KTKQVMVLF I TNGKYKRVKS LAAKAFKLYA DSYALRKNET SK 352

<212> Type : PRT
<211> Length : 352
SequenceName : SEQ ID 220
10 SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
15 <400> PreSequenceString :
MKKKIALAAL SFVSAAVLAA CSSAPGGSSD AAGNKIGDTV KIGYNLELSG DVAAYGQAEK 60
NGANLAVEEI NKAGGIDGKK IKVISKDNKS DNGEASTIST NLATQSKVNA ILGPATSGAT 120
AAAAPNANDA AVPLIVTPSGT QDNLTYSKKG VQDYIFRTTF QDSFQGGKIIA KYATDNLKAK 180
KVALYYDKSS DYAQGIADAF KKAYKGKITV EDTFQAKQD FQAALTKFKN KDFDAIVIPG 240
20 YYTETGLITK QARDMGLTQP ILGPDGFNDE KYVEGAGAAN TNNVHYVSGY STKVALTNKA 300
BKFLKDYKAK YGEEPNMFAA LAYDSVYMLA DAAKDAKTSK DIATNLAKLK NFKGVTGKMT 360
IDKKHNPVKS AVMVGLKDGK EDTATAVEAK 390
<212> Type : PRT
<211> Length : 390
25 SequenceName : SEQ ID 221
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
30 <400> PreSequenceString :
MKKLSLLLLV CLSLLGLFAC TSKKTADKKL TVVATNSIIA DITKNIAGNK VVLHSIVPVG 60
RDPHEYEPLP EDVKKTSQAD VIFYNGINLE NGGNAWFTKL VKNNAHKTKD DYFAVSDSVK 120
TIYLENAREK GKEDPHAWLD LKNGIYAKN IMKRLSEKDP KNKSYYQKNF QAYSAKLEKL 180
35 HKVAKEKISR IPTCKMIVT SEGCFKYFSK AYDIPSAYIW EINTEEEGTP NQIKALVKKL 240
RKSRVSALFV ESSVDDRPMK TVSKDTGIPI AAKIFTDSVA KKGQAGDSYY AMMKWNIDKI 300
ANGLSQ 306
<212> Type : PRT
<211> Length : 306
40 SequenceName : SEQ ID 222
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
45 <400> PreSequenceString :
MFVHTTKTKK RKWQRKVFL LLLFLLPIVS VLAFIGVFIG GGTAEASHDVE ATTGGVKLSA 60
KQFADKTKLG ISEEEAKNAL AFADRLMSRH HFTAQATAGV LAVGFRESGF DVKAVNNSGG 120
VAGFFQWGW GSSVNGDRWK VASKRELTE VEVDLMSTEL DGRYADVVKK VGSATDEKQA 180
50 AKDWSQYYEG VAVSDGQTKA DKIESWATTI CEALKSGGTN YAKVNNTGTS STAIPOGWEN 240
ISAFDGHAYE GSENVPOGQC TWYVYNRAKQ LGVSFSPYMG NGGQWYQVQG YHSSHTPKAH 300
TALS FVNGQA GSDPTYGHVA FVEAVKDDGS ILISEMNVYG QPAMTVAYRT FDAETAKQFW 360
YVEGK 365
<212> Type : PRT
55 <211> Length : 365
SequenceName : SEQ ID 223
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
60 <400> PreSequenceString :
MKMKRKL LSL VSVLTILLGA FWVTIKIVKAD QVTNYTNTAS ITKSDGTALS NDPSKAVNYW 60
EPLSFSNSIT FPDEVSIGAG DTLTIKLPEQ LQFTTALTFD VMHTNGQLAG KATTDPN'TGE 120
65 VTVTFTDIFE KLPNDKAMTL NFNAQLNHN ISIPGVVNFN YNNVAYSSYV KKDITPISP 180
DVNKVGYQDK SNPGLIHWKV LINNKQGAID NLTLTDVUGE DQETVKDSL V AARLQYIAGD 240
DVDSLDEAAS RPYAEDFSKN VTYQTNDLGL TTGFTYTIPG SSNNAIFISY TTRLTSSQSA 300

GKDVSNITIAI SGNNINYSNQ TGYARIESAY GRASSRVKRQ AETTTVTETT TSSSETTTS 360
EATTETSSST NNNSTTTETA TSTTGASTTQ TKTTASQTNV PTTTNIITTS KQVTKQKAKF 420
VLPSTGEQAG LLLTTTVGLVI VAVAGVYFYR TRR 453
<212> Type : PRT
5 <211> Length : 453
SequenceName : SEQ ID 224
SequenceDescription :

Sequence

10 <213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MTFKKLVLGL LSFVAVFTLV ACSSSNSKNL QDDIKEKKKL VVAVSPDYAP FEFKALVNGK 60
DTVVGADIDL AKAIKAKELGV KLELSSMSFD NVLSSLKTGK ADIAISGLSY TKERAQAYDF 120
15 SEAYYKTENA ILIKKSDLNK YTMISFNNK TKVAVQKGTI EEGLAKNQLK QSNITSLTSM 180
GEAVNELKSG QVDAIDLEKP VAEGYVSQNS DLVLAKVALK TEGGDAKAVA LPKDSGQLVK 240
TVNKVIKKLK KEDKYKQFIS DAVKLTGQQV D 271
<212> Type : PRT
<211> Length : 271
20 SequenceName : SEQ ID 225
SequenceDescription :

Sequence

25 <213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKHFFMTFS LLLAAVFLVA CSNLSDSGQR NWDKINKRGM LKIATAGTLY PQSYHDDHNNK 60
LTGYDVEILK EIGKRLGLKV QFTEMGVDGM LTAIKSGQID VANYSLEDGN KNISKFLRTS 120
PYKYSFTSMV VRSKDDSGIH SWSDLKGKKA AGAASNMYK IAKKLGAKLV VYDNVTNDVY 180
30 MKDLVNGRTD VIINDYYLQK IAVAAVKDKY AIKINQGLYA NPYSTSFTLS LKNKVLQKKI 240
NKAVKDMRKD GTLTKLSKKF FQGEDVTKKH YNSYKKIDIS DVD 283
<212> Type : PRT
<211> Length : 283
SequenceName : SEQ ID 226
35 SequenceDescription :

Sequence

40 <213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKLLKKMMQV ALATFFFGLL GTSTVFADDS EGWQFVQENG RTYYKKGALK ETYWRVIDGK 60
YYYFDPLSGE MVVGWQYIPA PHKGVITGPS PRIEIALRPD WFYFGQDGV L QEFVGKQVLE 120
AKTATNTNKH HGEEYDSQAE KRVYFEDQR SYHTLKTGWI YEEGYWYYLQ KDGGFDSRIN 180
RLTVGELARG WKDYPLTYD BEKLKAAPWY YLDPATGWQN LGNKWYYLRS SGAMATGWYQ 240
45 EGSTWYYLNA SNGDMKTGW F QVNGNWYYAY DSGALAVNTT VGGYYLNYNG EWWK 294
<212> Type : PRT
<211> Length : 294
SequenceName : SEQ ID 227
50 SequenceDescription :

Sequence

55 <213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKLLKKMMQV LLAVFFFGLL ATNTVFANTT GGRFVDKDNR KYYVKDDHKA IYWHKIDGKT 60
YYFGDIGEMV VGWQYLEIPG TGYRDNLF DN QPVNEIGLQE KWWWFGQDGA LLEQTDKQVL 120
EAKTSENTGK VYGEQYPLSA EKRTYYFDNN YAVKTGWIYE DGNWYYLNKL GNFGDDSYNP 180
LPIGEVAKGW TQDFHVTIDI DRSKPAPWYY LDASGKMLTD WQKVNGKWYY FGSSGSMATG 240
60 WKYVRGKWWY LDNKN GDMKT GWQYLG NKWY YLRSSGAMVT GWYQDGLTWY YLNAGNGDMK 300
TGWFQVNGKW YYAYSSGALA VNTTVDGYSV NYNGEWWQ 338
<212> Type : PRT
<211> Length : 338
SequenceName : SEQ ID 228
65 SequenceDescription :

Sequence


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<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
5 MNKKKMILTS LASVAILGAG FVASQPTVVR AEESPVASQS KAEKDYDAAK KDAKNAKKAV 60
  EDAQKALDDA KAAQKKYDED QKKTEEKAAL EKAASEEMDK AVAAVQQAYL AYQQATDKAA 120
  KDAADKMIDE AKKREEEAKT KFNTVVRAMVV PEPEQLAETK KKSEEAQKKA PELTKKLEEA 180
  KAKLEEAEEK ATEAKQKVDA EEVAPQAKIA ELENQVHRLE QELKEIDESE SEDYAKEGFR 240
  APLQSKLDAK KAKLSKLEEL SDKIDELDAE IAKLEDQLKA AEENNNVEDY FKEGLEKTIA 300
  AKKAELEKTE ADLKKAVNEP EKPAPAPETP APEAPAEQPK PAPAPQPAPA PKPEKPAPQP 360
10 KPEKTDQQA EEDYARRSEE EYNRLTQQQP PKAEKPAPAP KTGWKQENGM WYFYNTDGS 420
  ATGWLQNNGS WYYLNSNGAM ATGWLQYNGS WYYLNANGAM ATGWAKVNGS WYYLNANGAM 480
  ATGWLQYNGS WYYLNANGAM ATGWAKVNGS WYYLNANGAM ATGWLQYNGS WYYLNANGAM 540
  ATGWAKVNGS WYYLNANGAM ATGWVKDGD T WYYLEASGAM KASQWFKVSD KWYYVNGLGA 600
  LAVNTTVDGY KVNANGEWV 619
15 <212> Type : PRT
  <211> Length : 619
      SequenceName : SEQ ID 229
      SequenceDescription :

20 Sequence
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  <213> OrganismName : Streptococcus pneumoniae R6
  <400> PreSequenceString :
25 MKILPFIARG TSYLLKMSVK KLVPFLVVGL MLAAGDSVYA YSRGNGSIAR GDDYPAYYKN 60
  GSQEIDQWRM YSRQCTSFVA FRLSNVNGFE IPAAYGNANE WGHRRAREGY RVDNPTTIGS 120
  ITWSTAGTYG HVAWVSNVMG DQIEIEEYNY GYTESYNKRIV IKANTMTGFI HFKDLDSGSV 180
  GNSQSSASTG GTHYFKTKSA IKTEPLVSAT VIDYYPGEEK VHYDQILEKD GYKWLSTAY 240
  NGSYRYVQLE AVNKNPLGNS VLSSTGGTHY FKIKSAIKTE PLVSATVIDY YYPGEKVHYD 300
  QILEKDGKWK LSYTAYNGSR RYIQLEGVTS SQNYQNQSGN ISSYGSNNSS TVGWKKINGS 360
30 WYHFKSNGSK STGWLKDGSS WYYLKLSEGM QTGWLKENG S WYYLGSSGAM KTGWYQVSGE 420
  WYYSYSSGAL AINTTVDGYR VNSDGERV 448
  <212> Type : PRT
  <211> Length : 448
      SequenceName : SEQ ID 230
      SequenceDescription :

35 Sequence
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  <213> OrganismName : Streptococcus pneumoniae R6
  <400> PreSequenceString :
40 MFASKSERKV HYSIRKFSIG VASVAVASLV MGSVVHATEN EGSTQATSS NMAKTEHRKA 60
  AKQVVDEYIE KMLREIQDLR RKHTQNVALL IKLSAIKTKY LRELNVLEEK SKDELPLSEIK 120
  AKLDAAEFKF KKDITLKPGEK VAEAKKKVEE AKKKAEDQKE EDRRNYPTNT YKTLELEIAE 180
  FDKVKKEAEL ELVKKEAKES RNEGTLKQAK EKVESKKAEE TRLENIKTDR KKAEEEAARK 240
45 ADAKLKEANV ATSDQGKPKG RAKRGVPGEL ATPDKKENDA KSSDSSVGEE TLPSSSLKSG 300
  KKVAAEAEKKV EEAEEKAKDQ KEEDRRNYPT NTYKTLDEI AESDVKVKEA ELELVKEEAK 360
  EPRDEEKIKQ AKAKVESKKA BATRLENIKT DRKKAEEEA RKAEEEDKVK EKPAPQPAPA 420
  PATQPEKPAP KPEKPAPQPK AEKTDQQAEE EYARRSEEE YNRLTQQQPP KTEKPAQPST 480
  PKTGWKQENG MWYFYNTDGS MATGWLQNNG SWYYLNANGA MATGWLQNNG SWYYLNANGS 540
50 MATGWLQNNG SWYYLNANGA MATGWLQYNG SWYYLNSNGA MATGWLQYNG SWYYLNANGD 600
  MATGWLQNNG SWYYLNANGD MATGWLQYNG SWYYLNANGD MATGWVKDGD TWYYLEASGA 660
  MKASQWFKVS DKWYYVNGSG ALAVNTTVDG YGVNANGEWV N 701
  <212> Type : PRT
  <211> Length : 701
      SequenceName : SEQ ID 231
      SequenceDescription :

60 Sequence
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  <213> OrganismName : Streptococcus pneumoniae R6
  <400> PreSequenceString :
  MKKTTILSLT TAAVILAAYV PNEPILAAVY PNEPILADTP SSEVIKETKV GSIIQQNNIK 60
  YKVLTVENGI GTVQVGNVGT PVEFEAGQDG KPFTIPTKIT VGDVFTVTE VASQAFSYYP 120
  DETGRIVYYP SSIITPSSIK KIQKKGFHGS KAKTIIFDKG SQLEKIEDRA FDFSELEIE 180
65 LPASLEYIGT SAFSFSQKLE KLTFFSSSKL ELISHEAFAN LSNLEKLTLP KSVKTLGSNL 240
  FRLTTLKLV DVEEGNESFA SVDGVLFSD KTQLIYPSQ KNDESYPKPK ETKELASYSF 300
  NKNSYLKLE LNEGLEKIGT FAFADAIKLE EISLPNSLET IERLAFYGNL ELKELILPDN 360
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VKNFGKHVMN GLPKFLTLTG NNINSLPSFF LSGVLDLKE IHIKNKSTEF SVKKDTFAIP 420
ETVKFYVTSE HIKDVLKSNL STSNDIIVEK VDNIKQETDV AKPKKNSNQ VVGWVKDKGL 480
WYYLNEGSM ATGWVKDKGL WYYLNEGSM ATGWVKDKGL WYYLNEGSM ATGWVKDKGL 540
WYYLNEGSM ATGWVKDKGL WYYLNEGSM ATGWVKDKGL WYYLNEGSM ATGWVKDKGL 600
5 WYYLNEGSM ATGWVKDKGL WYYLNEGSM ATGWVKDKGL WYYLNEGSM ATGWVKVSGK 660
WYYTYNSGDL LVNTTTPDGY RVNANGWVG 690
<212> Type : PRT
<211> Length : 690
SequenceName : SEQ ID 232
10 SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
15 <400> PreSequenceString :
MEINVSKLRT DLPQGVQPY RQVHAHSTGN PHSTVQNEAD YHWRKDPELG FFSHIVGNGC 60
IMQVGPVDNG AWDVGGGUNA ETYAAVELIE SHSTKEEFMT DYRLYIELLR NLADEAGLPK 120
TLDTGSLAGI KTHEYCTNNQ PNNHSDHVDY YPYLAKWGIS REQFKHDIEN GLTIETGWQK 180
NDTGYWYVHS DGSYPKDKFE KINGTWYFYD SSGYMLADRW RKHTDGNWYW FDNSGEMATG 240
20 WKKIADKWYY FNEEGAMKTG WVKYKDTWYY LDKAEGAMVS NAFIQSADGT GWYYLKP DGT 300
LADRPEFTVE PDGLITVK 318
<212> Type : PRT
<211> Length : 318
SequenceName : SEQ ID 233
25 SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
30 <400> PreSequenceString :
MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAAARA HAAQQNGFEA 60
FAPFAAVLT AHATGNAGQA TVNTLAGLFI LFRALFIWCY IADKAALRSL MWVGGFVCTV 120
GLFVVAA 127
<212> Type : PRT
35 <211> Length : 127
SequenceName : SEQ ID 234
SequenceDescription :

Sequence

40 <213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNKIYRIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN ATDEDEEEEL 60
ESVQRSVVG IASMEGSGE LETISLSMTN DSKEFVDPYI VVTLKAGDNL KIKQNTNENT 120
45 NASSFTYSLK KDLTGLINVE TEKLSFGANG KKVNIISDTK GLNFAKETAG TNGDTTVHLN 180
GIGSTLDTL AGSSASHVDA GNQSTHYTRA ASIKDVLNAG WNIKGVKTGS TTGQSENVD 240
VRTYDTVEFL SADTKTTTVN VESKDNGKRT EVKIGAKTSV IKEKDGLVT GKKGENGSS 300
TDEGEGLVTA KEVIDAVNKA GWRMKT TAN GQTGQADKFE TVTSGTNVTF ASGKGTTATV 360
SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS SGKVISGNVS PSKGKMDTV 420
50 NINAGNNIEI SRNGKNIDIA TSMAPQFSSV SLGAGADAPT LSVDDGALN VGSKDANKPV 480
RITNVAPGVK EGDVTNVAQL KGVAQNLRN IDNVDGNARA GIAQAIATAG LVQAYLPKGS 540
MMAATGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY QW 592
<212> Type : PRT
55 <211> Length : 592
SequenceName : SEQ ID 235
SequenceDescription :

Sequence

60 <213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MLLAEGQKSA VTEYYLNHGT WPSNNSDAGV ASTATDIKKG YVKEVKVEKG VITATMLSSG 60
VNNEIKGKKL SLWAKRQAGS VKWFCGQPV E RAANNAANDA VTAATANGNG KIDTKHLPST 120
65 CRDAASAVCI ETPPTAFYKN T 141
<212> Type : PRT
<211> Length : 141

SequenceName : SEQ ID 236
SequenceDescription :

Sequence

5 <213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MKTDDKRTTE THRKAPKTGR IRFSPAYLAI CLSFGILPQA WAGHTYFGIN YQYYRDFAE 60
KGKFAVGAKD IEVYNKKGEL VGKSMTKAPM IDFSVVSRRNG VAALVGDQYI VSVAHNGGYN 120
10 NVDFGAEGRN PDQHRFSYQI VKRNNYKPDN SHPYNGDYHM PRLHKFVTDA EPVEMTSDMR 180
GNTYSDKEKY PERVRIGSGH HYWRYDDDKH GDLSYSGAWL IGGNTHMQGW GNNGVVSLSG 240
DVRHANDYGP MPIAGAAGDS GSPMFTYDKT NNKWLNLGVL QTGYPYSGRE NGFQLIRKDW 300
FYDDIYRGDT HTVFFEPFRSN GHFSFTSNNN GTGTVTETNE KVSNNPKLVQ TVRLFDESIN 360
ETDKPEPVYAA GGVNQYRPRL NNGENLSFID YGNGKLILSN NINQGAGGLY FEGDFTVSPE 420
15 NNETWQAGAV HISEDSTVTW KVGNDVANDRL SKIGKGTLVH QAKGENQCSI SVGDGTIVLD 480
QQADDKGKKQ AFSEIGLVSG RGTVQLNADN QFNPDKLYFG FRGGRLDLNG HSLSFHRIQN 540
TDEGAMIVNH NATTTSTVTI TGNESITQPS GKNINRLNYS KEIAYNGWFG EKDTTKTNGR 600
LNLVYQPAAE DRTLILLSGGT NLNGNITQTN GKLEFFSGRPT PHAYNHLGSG WSKMEGIPQG 660
EIVWDNDWIN RTFKAENFHI QGGQAVISRN VAKVEGDWHL SNHAQAVFGV APHQSHTICT 720
20 RSDWTGLTNC VEKTTITDDKV IASLTKTDIS GNVSLADHAH LNLTLGLATLN GNLSANGDTR 780
YTVSHNATQN GNLSLVGNAQ ATFNQATLNG NTSASGNASF NLSNNAQNG SLTSLDNAKA 840
NVSHSALNGN VSLADKAVFH FENSRTGQQL SGSKDTALHL KDSEWTLPSG TELGNLNLNDN 900
ATITLNSAYR HDAAGAQTGS VSDTPRRRSR RSLSVTPPT SVESRENTLT VNGKLNQGT 960
FRFMSLEFGY RSDKLKLAES SEGTYTLAVN NTGNEPVSLD QLTVEGKDN KPLSENLNFT 1020
25 LQNEHVDAGA WRYQLIRKDG EFRHLNHPVKE QELSDKLGA EAKKQAEKDN AQLSDALIAA 1080
GRDAAEKTES VAEPARQAGG ENVGIMQAE EKKRVQADKD SALAQREAE TRPATTAFPR 1140
ARRARDLPQ PQPQPQPQPQ PQRDILSRYA NSGLSEFSAT LNSVFAVQDE LDRVFAEDRR 1200
NAVWTSGIRD TKHYRSQDFR AYRQQTDLRQ IGMQKNLGS RVGILFSHNR TENTFDDGIG 1260
NSARLAHGAV FGQYGIGRFD IGISTGAGFS SGLSDGIGG KIRRRVLHYG IQARYRAGFG 1320
30 GFGIEPYIGA TRYFVQKADY RYENVNIATP GLAFNRYRAG IKADYSFKPA QHISITPYLS 1380
LSYTDAASGK VTRRVNTAVL AQDFGKTRSA EWGVNAEIKG FTLSLHAAAA KGPQLEAQHS 1440
AGIKLGYRW 1449

<212> Type : PRT
<211> Length : 1449
35 SequenceName : SEQ ID 237
SequenceDescription :

Sequence

40 <213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV SEAILLAEGQ KSAVTEYYLN 60
HGEWPSNNTS AGVASSTDIK GKYVQSVVEK NGVVTATMAS SNVNNEIKGK KLSLWAKRQD 120
GSVKWFCCQP VKRNDTATTN DDVKADTAAN GKQIDTKHLP STCRDAASAG 170
45 <212> Type : PRT
<211> Length : 170
SequenceName : SEQ ID 238
SequenceDescription :

Sequence

50 <213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAQVK DMDLQALHGR 60
55 KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT DYTYPREYET AETTSGLTGT 120
LTTSLSTLNA PALSRQSDG SGSKSSLGLN IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF 180
FLRGIDVVSP ANADTDVFIN IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL 240
IKPKTNAFEA AYKENYALWM GPYKVSKGK PTEGLMVD FS DIQPYGNHMG NSAPSVEADN 300
SHEGYGSDE AVRRHRQGP 320
60 <212> Type : PRT
<211> Length : 320
SequenceName : SEQ ID 239
SequenceDescription :

Sequence

65 <213> OrganismName : Neisseria meningitidis Z2491

<400> PreSequenceString :
MRPIFLSFVL FPILITACST PDKSARWENI GTISNGNIHT YINKDSVRKN GNLMIQDKK 60
VVTNLKQERF ANTPAYKTAI AEWEIHCNNK TYRLSSLQLF DTKNTEISTQ NYTASSLRPM 120
SILSGTLTEK QYETVCGKKL 140

5 <212> Type : PRT
<211> Length : 140
SequenceName : SEQ ID 240
SequenceDescription :

10 Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNKLFITALS ALALSACAGT WEGAKQDTAR NLDKTQAAAE RAAEQTGNV EKGWDKTKEA 60
15 VKKGGNAVGR GISHLGGKIE NATE 84
<212> Type : PRT
<211> Length : 84
SequenceName : SEQ ID 241
SequenceDescription :

20 Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
25 MKLLFIPLVL FVAVEHFYIA WLEMTQIPSE KAAETFKLPY EFMEQNRVQT LFGNQGLYNG 60
FLGIGLVWSR FAAPDNAVYG ATVLFLGFVL IAAAWGAFSS GNKGILVKQG LPAFLAAAV 120
LAV 123
<212> Type : PRT
<211> Length : 123
30 SequenceName : SEQ ID 242
SequenceDescription :

Sequence

35 <213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MASSNVNNEI KDKKLSLWAK RQDGSVKWFC GQPVKRDAAT DADVTADSGN EIDTKHLPST 60
CRDAASAVCT KTPEYYPNHG EWPKNFVIPA QAGIQVCRHG NLSGKKVSPV LSSRFPLSWE 120

40 <212> Type : PRT
<211> Length : 120
SequenceName : SEQ ID 243
SequenceDescription :

45 Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MLLAEGQKSA VTEYYLNHGE WPSNNTSAGV ATSTDIKGY VQSVEVKNGV VTATMASSNV 60
50 NNEIKGKKLS LWAKRQDGSV KWFCGQPVKR NDTATTNDDV KADTAANGKQ IDTKHLPSTA 120
STRKSTPN 128
<212> Type : PRT
<211> Length : 128
SequenceName : SEQ ID 244
55 SequenceDescription :

Sequence

60 <213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MPIPFKPVLA AAALAQAFPA FAADPAPQSA QTLNEITVTG THKTQKLGE E KIRRKTLCLK 60
LVNDEHDLVR YDPGISVVEG GRAGSNGFTI RGVDKDRVAI NVDGLAQAES RSSEAFQELF 120
GAYGNFNANR NTSEPFNFSE VTITKGADSL KSGSGALGGA VNYQTKSASD YVSEDKPYHL 180
GIKGGSVGKN SQKFSSITAA GRLFGLDALL VYTRRFGKET KNRSTEGDIE IKNDGYVYNP 240
65 TDTGGPSKYL TYVATGVARS QPDPQEWVKN STLFLKGYNF NDQNRIGWIF EDSRTDRFTN 300
ELSNLWTGTT TSAATGDYRH RQDVSYYRRS GVEYKNELEH GPWDSLKLRY DKQRIDMNTW 360
TWDIPKNYDK RINGEVYHS FRHIRQNTAQ WTADFEKQLD FSKAVWAAQY GLGGGKGDNA 420

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NSDYSYFAKL YDPKILASNQ AKITMLIENR SKYKFAYWNN AFHLGGNDRF RLNAGIRYDK 480
NSSSAKDDPK YTTAIRGQIP HLGSERAHAG FSYGTGFDWR FTKHLHLLAK YSTGFRAPTS 540
DETWLLFPHP DFYLKANPNL KAEKAKNWEL GLAGSGKAGN FKLSGFKTKY RDFIELTYMG 600
VSSDDKNNPR YAPLSDGTAL VSSPVWQONQ RSAAWVKGIE FNGTWNLDSI GLPKGLHTGL 660
5 NVSYIKGKAT QNNGKETPIN ALSPWTAVYS LGYDAPSKRW GINAYATRTA AKKPSDTVHS 720
NDDLNNPWPY AKHSKAYTLF DLSAYLNIGK QVTLRAAAYN ITNKQYYTWE SLRSIREFGT 780
VNRVDNKTHA GIQRFTSPGR SYNFTIEAKF 810
<212> Type : PRT
<211> Length : 810
10 SequenceName : SEQ ID 245
SequenceDescription :

Sequence
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15 <213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MKKSLLIALLT AALPVAAMAD VTLYGTIKTG VETSRSEVEHN GGQVSVVETG TGIVDLGSKI 60
GFKGQEDLGN GLKAIWQVEQ KASIAGTDSG WGNRQSFGL KGGFGKLRVG RLNSVLKDTG 120
DINPWDSKSD YLGVNKIAEP EARLISVRYD SPEFAGLSGS VQYALNDNVG RHNSSESYHAG 180
20 FNYKNGGFFV QYGGAYKRHQ DVDDVKIEKY QIHRLVSGYD NDALYASVAV QQQDAKLVED 240
NSHNSQTEVA ATLAYRFGNV TPRVSYAHGF KGSVDDAKRD NTYDQVVVGA EYDFSKRTSA 300
LVSAGWLQEG KGENKFVATA GGVGLRHKF 329
<212> Type : PRT
<211> Length : 329
25 SequenceName : SEQ ID 246
SequenceDescription :

Sequence
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30 <213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MKTLLLLLIPL VLTACGTLTG IPAHGGGKRF AVEQELVAAS SRAAVKEMDL SALKGRKAAL 60
YVSVMGDQGS GNISGGRYSI DALIRGGYHN NPESATQYSY PAYDTTATTK SDALSSVTTS 120
TSLLNAPAAA LTKNSGRKGE RSAGLSVNGT GDYRNETLLA NPRDVSFLTN LIQTVFYLRG 180
35 IEVVPPEYAD TDVVFVTVDF GTVRSRTELH LYNAETLKAQ TKLEYFAVDR DSRKLLIAPK 240
TAAYESQYQE QYALWMPYS VGKTVKASDR LMVDFSDITP YGDTTAQNRP DFKQNGKKP 300
DVGNEVIRRR KGG 313
<212> Type : PRT
<211> Length : 313
40 SequenceName : SEQ ID 247
SequenceDescription :

Sequence
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45 <213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNKTLILPV AILLGGCAAG GGNTFGSLDG GTGMGGSIVK MAVESQCRAE LNKRESEWRLT 60
ALAMSAEKQA EWENKICACV AQEAPNQLTG NDVMQMLDPS TRNQALAAIT AKTVSACFKH 120
LYR 123
50 <212> Type : PRT
<211> Length : 123
SequenceName : SEQ ID 248
SequenceDescription :

Sequence
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55 <213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNPLIHQAKE SSMQTRILSA VLLAFSTAAF AGGAFTLQFD NPSEDGGFTQ NQILSAPYGF 60
GCSGGNASPA LSWKNPPAGT KSFVLTVYDK DAPTGLGWMH WVADIPADV RRRNATSLQL 120
SRCASIADDQ SAAISAVISL QICRIRLTPS YTAKMPSPCC NHANTPQSAA SAALCGTSSS 180
VSTAAA 186
60 <212> Type : PRT
<211> Length : 186
SequenceName : SEQ ID 249
SequenceDescription :

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Sequence

<213> OrganismName : Neisseria meningitidis Z2491

<400> PreSequenceString :

5 MNKTLKRRVF RHTALYAAIL MFSHTGGGGG AMAQTRQYAI IMNERNQPEV QWNGSYSIKD 60
KDRKREYTHH NHQQGGSSVS FNNSEDELVSQ QSGTAVFGTA TYLPPYGVKS GFDAALAKER 120
NNAVDWIHTT HPGLIGYSYD GVVCRSATDC PKLVYKTRFS FDNPDIAKTG GGLDKHTEPS 180
RDNSPIYKLL DHPWLGVSFN LGAEGIAKNG KTINKLVSSF NEKNSNNNLV YTEGRDISL 240
10 GNWQRETTAM AYYLNAKLHL LDKKQIQNIT DKTQVLGVK PSIDVTRNT GTAGILSYWA 300
KWDIKDTGQI PVKLSLTQVK AGRCVNKDNF NKNTKTSSPA LTAPALWFGA GQDGKAEMYS 360
ASVSTYDPSS SSRIFLQNLK RKTDTSRPGR YSLATLNKSD IESREPSFTS RQTVIRLDGG 420
VQQIKLDRNN TEVTGFNGND GKNDTFGIVS EGSFMPDASE WKKVLLPWTV RAFNYDGRFN 480
TVNKEENNGK PKYSQKYRSR NNGKHERNLG DIVNSPIVAV GEYLATSAND GMVHIFKQSG 540
GDKRSYNLKI SYIPGTMPRK DIESKDSTLA KELRAFAEKG YVCDRYGVDG GFVLRRTTDD 600
15 QDKQKHFFMF GAMGLGGRGA YALDLTKADD NDPTKASLFD VKDNGNNGNN GNNRVELGYT 660
VGTPQIGKTH NGKYAAFLAS GYATKQIDSG ENKTALVYVD LESNNGTLIR KIEVTDGKGG 720
LSSPTLVDDK LDGTVDIAYA GDRGGKMYRF DLSGNNPNSW TVRTIFQGTK PITSAPAIISQ 780
LKDKRVDVIFG TGSDDLSEDDV LSTDEQHIYG IFDNDTNTGT AQEGLGKGLL EQKLSEENKT 840
LFLTDYKRSD GSGDKGWVVK LKDGQRVTVK PTVVLRATFV TIHKYTGNDK CGAETAILGI 900
20 NTADGGKLTG KSARPIVPA NSKVAQYSGD KKTSSGKSIP IGCMEKDDGT VCPNGYVYDK 960
PVNVRYLDEK KTDGFSTTAD GDAGGSGTFK EGKKPARNNR CFSGKGVRTL LMNDLDSLDI 1020
TGPMMGMRRI SWREVFY 1037

<212> Type : PRT

<211> Length : 1037

25 SequenceName : SEQ ID 250
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491

<400> PreSequenceString :

30 MKHPKLTLLA ALLTTAATAA PLPVVTSFSI LGDVAQKIGG ERVSIQSLVG ANQDTHAYHM 60
TSGDIKKIRS AKLVLLINGL LEAADIQRAV KQSKVSYAEA TKGIQPLKAE EGGHHHDHD 120
HDHHDHDEGH HHDHGEYDPH VWNDPVLMAS YQNVAEALI KADPEGKVYY QQLGNYQMQ 180
35 LKKLHSDAQA AFNAVPAKR KVLTHGDAFS YMCKRYHIEF IAPQVSSEA EPSAKQVAAI 240
IRQIKREGIK AVFTENIKDT RMVDRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHNIK 300
ALTNAMKQ 308

<212> Type : PRT

<211> Length : 308

40 SequenceName : SEQ ID 251
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232

<400> PreSequenceString :

45 MKKRILSAVL VSGVTILGAAT TVGAEDLSTK IAKQDSIISN LTTEQKAAQN QVSALQAQVS 60
SLQSEQDKLT ARNTELEALS KRFEQETKAL TSQIVARNEK LKNQARSAYK NNETSQYINA 120
LLNSKSISDV VNRLVAINRA VSANAKLLEQ QKADKVSLEE KQANQTAIN TIAANMAMAE 180
50 ENQTLRTTQQ ANLEAATANL ALQLASATED KANLVAQKEA AEKAAAEALA QEQAQKVAQ 240
EQAAQQAASV BAAKSAITPA PQATPAAQSS NAIEPAALTA PAAPSARPQT SYDSSNTYPV 300
GQCTWGAKSL APWAGNNWGN GGQWYSAQA AGYRTGSTPM VGAIWVNDG GYGHVAVVVE 360
VQSASSIRVM ESNYSGRQYI ADHRGWFNPT GVTFIYPH 398

<212> Type : PRT

<211> Length : 398

55 SequenceName : SEQ ID 252
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232

<400> PreSequenceString :

60 MITIKNPKIL KWLKYVLSAI LSLIILVIII GGLLFTFYIS SAPKLSEAQL KSTNSSLVYD 60
GNNNLIAIDL SEKRENTVAD SIPINLVNAI TSIEDKRFFN HRGVDLYRIF GAAFNHLSQ 120
65 TTQGGSTLDQ QLIKLAYFST NESDQTLKRK AQEVWLALQM ERKYTKQEL TFIYINKVYM 180
NGNYGMLTAA KSYYGKDLK LSYAQLALLA GIPQAPSQYD PYLHPEAAQN RRNVVLQQMY 240
MEKHLTKAEY ETAIATPVAE GLQSLQQRST YPKYMDNYLK QVIEEVKKET NKDIFTAGLK 300

VYTNIIPDAQ QTLYNIYHSG DYVYYPDQDF QVASTIVDVT NGHVIQQLGG RNQDENVSFG 360
TNQAVLTDRD WGSTMKPITA YAPAIESGVY TSTAQSTNDS VYYWPGTTTQ LFNWDLRYNG 420
WMTIQAAIML SRNVPVAVRAL EAAGLDYARS FLSSLGINYP EMHYSNAISS NNSSSDKKYG 480
ASSEKMAAAY AAFANGGIYH KPRYVKNVEF SDGTSKTFDE KGKRAMKETT AYMMTDMLKT 540
5 VLTYGTGTAA AIPGVAQAGK TGTSNYTDEE LAKIGEKYGL YPDYVGTLAP DENFVGFTKR 600
YAMAVWTGYK NRLTPVYGSS LEIASDVYRS MMTYLTNGYS EDWTMPNGLY RSGGFLYLSG 660
TYASNTDYTN SVYNNLYSNM TTTASSQTTS DDTSSSNDTS NSTNTDNNGS HPSTDDKKT 720
H 721
<212> Type : PRT
10 <211> Length : 721
SequenceName : SEQ ID 253
SequenceDescription :

Sequence
15 -----
<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MIITKSLFV TSVALSLAPL VTAQAQEWTP RSVTEIKSEL VLVDNVFTYT VKYGDTLSTI 60
AEAMGIDVHV LGDINHIANI DLIFPDILT ANYNQHQQAT TLTVQAPASS PASVSHVPSS 120
20 EPLPQASATS QSTVPMAPSA TPSDVPTTPL ASAKPDSFVT ASSELTSSSTN DVSTELSSSES 180
QKQPEVSQEA VPTPKAAETT EVEPKTDISE DPTSANRPVP NESASEEASS AAPAQAPAEK 240
EETSQMLTAP AAQKAVADTT SVATSNGLSY APNHAYNPMN AGLQPQTAAF KEEVASAFGI 300
TSFSGYRPGD PGDHGKGLAI DFMVPVSSTL GDQVAQYAIH HMAERGISYV IWKQRFYAPF 360
ASIYGPAYTW NMPMDRGSIT ENHYDHVHVS FNA 393
25 <212> Type : PRT
<211> Length : 393
SequenceName : SEQ ID 254
SequenceDescription :

Sequence
30 -----
<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MKKKILLMMS LISVFFAWQL TQAKQVLAEG KVKVVTTFYP VYEFTKGIVG NDGDVSMMLK 60
35 AGTEPHDFEP STKDIKKIQD ADAFVYMDN METWVSDVKK SLTSSKVTIV KGTGNMLLVA 120
GAGHDHHHED ADKKHEHNKH SEEGHNHAFD PHVWLSPYRS ITVVENIRDS LSKAYPEKAE 180
NFKANAATYI EKLKELDKDY TAALSDAKQK SFVTQHAAFG YMALDYGLNQ ISINGVTPDA 240
EPSAKRIATL SKYVKYGIK YIYFEENASS KVAKTLAKEA GVKA AVLSP L EGLTKKEMKA 300
GQDYFTVMRK NLETLRLTTD VAGKEILPEK DTTKTVYNGY FKDKVKDRQ LSDWSGWSQS 360
40 VYPYLQDGT L DQWWDYKAKK SKGKMTAEY KDYYTTGYKT DVEQIKINGK KKTMTFVRNG 420
BKKTFTYTYA GKEILTYPKG NRGVRFMFEA KEPNAGEFKY VQFSDHAIAP EKAHFHLYW 480
GGDSQEKHLK ELEHWPTYG SDLSGREIAQ EINAH 515
<212> Type : PRT
<211> Length : 515
45 SequenceName : SEQ ID 255
SequenceDescription :

Sequence
50 -----
<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MKKFHRFLVS GVILLGFNGL VPTMPSTLIS QQENLVHAAV LGDNYPSKWK KNGIDSWNM 60
YIRQCTSFSA FRLSSANGFQ LPKGYNACT WGHIKNQGY PVNKTPSIGA IAWFDKNAYQ 120
SNAAYDHVAW VADIRGDTV IEEYNYNAGQ GPERYHKRQI PKSQVSGYIH FKDLSSQTSH 180
55 SYPRQLKHIS QASFDPSGTY HFTTRLPVKG QTSIDSPDLA YVEAGQSVYV DKVVVTAGGYT 240
WLSYLSFSGN RRYIPIKEPA QSVVQNDNTK PSIKVGDTV FPGVFRVDQL VNNLIVNKEL 300
AGGDPTPLNW IDPTPLDET D NQGVKVLGNQI LRVGEYFTVT GSYKVLKIDQ PSNGIYVQIG 360
SRGTWVNADK ANKL 374
<212> Type : PRT
60 <211> Length : 374
SequenceName : SEQ ID 256
SequenceDescription :

Sequence
65 -----
<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :

MLKFTSNILA TSVAETTQVA PGGCCCCCTT CCFSIATGSG NSQGGSGSYT PGK

<212> Type : PRT

<211> Length : 53

5 SequenceName : SEQ ID 257
 SequenceDescription :

Sequence

10 <213> OrganismName : Streptococcus pyogenes MGAS8232

<400> PreSequenceString :

MGESYSVEAV	LTAVDKTFGK	TLQSAIRSIE	GLEKRSTGFS	SVSQKASSMF	KSMLGANLAG	60
QAISAMTRTV	SSGLGSMLGE	MNSSAKAWKT	FDANLADIGF	GKKQILAVKT	AMQDYATKTI	120
YSASDMASTY	AQLAAVGVD	TGKLVKAFGG	LAASAENPKQ	AMKSISQMT	QAVGRPTVAW	180
15 QDFRIMLEQT	PAGMAKVAKS	MGKNLDELVA	DIQAGRVKTS	DFLEAVKKAG	NDKSFQKMAT	240
EFKTVDAQID	GMREGLSNKL	QPAFEKVNQF	GIRAIEAIGK	QLDKVDFSKF	ASNLGKFLEG	300
INIDKIVSNI	SSAVSSVTISK	VKEFWDFGFKQ	TGAISAFSGA	LQSVWGALKN	VASAMSGGNW	360
KTFGATVGGI	VKHVSNFAKA	VSDVLGKMDP	GRLRSWIATF	AAVAGGFKLF	EKLTGQSVIG	420
SFLDKIGSKF	GLFGNKAKEG	TDKASNGARR	SGGIISQIFS	GLGNIVKSAG	TAISTAAGKI	480
20 GVGIKTALSG	IPPYH					495

<212> Type : PRT

<211> Length : 495

SequenceName : SEQ ID 258

SequenceDescription :

Sequence

25 <213> OrganismName : Streptococcus pyogenes MGAS8232

<400> PreSequenceString :

30 MKKGFFLMVM	VVSLVMIAGC	DKSANPKQPT	QGMSVVSIFY	PMYAMTKEVS	GDLNDVRMIQ	60
SGAGIHSFEP	SVNDVAAIYD	ADLFVYHSHT	LEAWARLDLP	NLKKSKVDVF	EASKPLTLDR	120
VKGLEDEMEVT	QGIDPATLYD	PHTWTDPLVA	GEEAVNIAKE	LGRLDPKHKD	SYTKNAKAFK	180
KEAEQLTEBY	TQRFKKVRSK	TFVTQHTAFS	YLAKRFGLKQ	LGISGISPEQ	EPSPRQLKEI	240
QDFVKEYNVK	TIFAEQNVNP	KIAHAIAKST	GAKVKTLSPL	EAAPSGNKTY	LENLRANLEV	300
35 LYQQLK						306

<212> Type : PRT

<211> Length : 306

SequenceName : SEQ ID 259

SequenceDescription :

Sequence

40 <213> OrganismName : Streptococcus pyogenes MGAS8232

<400> PreSequenceString :

45 MEKKQRFSLR	KYKSGTFSVL	IGSVFLMMTT	TVAADELSTM	SEPTITNHTQ	QQAQHLTNTE	60
LSSAESKSD	TSQITPKTNR	EKEQPQGLVS	EPTTTELADT	DAAPMANTGP	DATQKSASLP	120
PVNTDHDVW	KTGAWDKGY	KGQGVVAVI	DTGIDPAHQS	MRISDVSTAK	VKSKEDMLAR	180
QKAAGINYGS	WINDKVFFAH	NYVENSNDIK	ENQFEDFDED	WENFEFDAEA	EPKAIKKHKI	240
YRPQSTQAPK	ETVIKTEETD	GSHDIDWTQT	DDDTKYESHG	MHVTGIVAGN	SKEAAATGER	300
50 FLGIAPEAQV	MFMRVFANDV	MGSAESLFIK	AIEDAVALGA	DVINLSLGT	NGAQLSGSKP	360
LMEAIEKAKK	AGVSVVVAAG	NERVYGSDDH	DPLAINPDYG	LVGSPSTGRT	PTSVAAINSK	420
WVIQRLMTVK	ELENRADLNH	GKAIYSESVD	FKNIKDSLGY	DKSHQFAYVK	ESTDAGYKAQ	480
DVKDKIALIE	RDPNKTYDEM	IALAKKHGAL	GVLIFFNNKPG	QSNRSMRLTA	NGMGIPSAFI	540
SHEFGKAMSQ	LNGNGTGSLE	FDSVVSKAPS	QKGEMNHFHS	NWGLTSDGYL	KPDITAPGGD	600
55 IYSTYNDNHY	GSQTGTSMAS	PQIAGASLLV	KQYLEKTQPN	LPKEKIADIV	KNLLMSNAQI	660
HVNPETKTTT	SPRQQAGALL	NIDGAVTSGL	YVTGKDNYS	ISLGNITDTM	TFDVTVHNLS	720
NKDKTLRYDT	ELLTDHVDPO	KGRFTLTSTRS	LKTYQGGEVT	VPANGKVTVR	VTMDVSQFTK	780
ELTKQMSNGY	YLEGFVRFRD	SQDDQLNRVN	IPFVFGKQF	ENLAVAEESI	YRLKSQKGTG	840
FYFDESGPKD	DIYVGKHFTG	LVTLGSETNV	STKTISDNGL	HTLGTGKNAD	GKFILEKNAQ	900
60 GNPVLATSPN	GDNNQDFAAF	KGVFLRKYQG	LKASVYHASD	KEHKNPLWVS	PESFKGDKNF	960
NSDIRFAKST	TLLGTAFSGK	SLTGAELPDG	YYHYVVSYP	DVVGAKRQEM	TFDMILDRQK	1020
PVLSQATFDP	ETNRFKPEPL	KDRGLAGVRK	DSVFYLERKD	NKPYTVTIND	SYKYVSVEDN	1080
KTFVERQADG	SFILPLDKAK	LGDFYYMVED	FAGNVAIAKL	GDHLPQTLGK	TPIKLKLTDG	1140
NYQTKETLKD	NLEMTQSDTG	LVTNQAQLAV	VHRNQPSQL	TKMNQDFFIS	PNEDGNKDFV	1200
65 AFKGLKNVY	NDLTVNVYAK	DDHQKQTPIW	SSQAGASASA	IESTAWYGIT	ARGSKVMPGD	1260
YQYVVYTRDE	HGKEHQKQYT	ISVNDKKPMI	TQGRFDTING	VDHFTPDKTK	ALGSSGIVRE	1320
EVFYLAKKNG	RKFDVTEGKD	GITVSDNKMY	IPKNPDGSYT	ISKRDGVTLS	DYYVYLVEDRA	1380

GNVSFATLRD LKAVGKDKAV VNFGLDLPVP EDKQIVNFTY LVRDADGKPI ENLEYNNNSG 1440
NSLILPYGKY TVELLTYDTN AAKLESDDKIV SFTLSADNNF QQVTFKMTML ATSQITAHFD 1500
HLLPEGSRSV LKTAQGQLIP LEQSLYVPKA YGKTVQEGTY EVVVSPLPKGY RIEGNTKVNT 1560
LPNEVHELSSL RLVKVGDAASD STGDHKVMSK NNSQALTAFA TPTKTTTSAT AKALPSAGEK 1620
5 MGLKLRIVGL VLLGLTTCVFS RKKSTKD 1647
<212> Type : PRT
<211> Length : 1647
SequenceName : SEQ ID 260
SequenceDescription :
10 Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
15 MMRSLSFGVS GMQNHQTRMD VIGNNVANVN TTGFKRGRVN FQDLISQQLS AAARPNEEVG 60
GVNPKFVGLG VLIASIDTVH TQALQTTGI NTDVSIQSG FFLVKSSEKT FFTRAGAFGV 120
DNAGTLVNPA NGMRVQGWMA QDVAGERLIN SSAQTQDLVI PIGQKIDAQQ TSTVHYACNL 180
DKRLPELAAD ANEADVRKST WTTDFQVYDS FGQHTLQIN FSRVPGTNNQ WQATVAVDPG 240
TEVDTQTRVG VGTSDGAANT FIVNFDNFGH LASVTDTAGN VTGPTQVLL EASYDVVGAN 300
20 PDDAGQVTRH AFTLNLGEIG TARNTTQFA ERSTTKAYRQ DGYAMGYLEN FKIDQSGVIT 360
GVYSGVVSQD IGQLALAGFA NQGGLEKAGE NTVVQSNNSG IANISTSGVM GKGLIAGTL 420
EMSNVDLTDQ FTDMIITQKG FQAGAKTIQT SDTMLDTVLS LKR 463
<212> Type : PRT
<211> Length : 463
25 SequenceName : SEQ ID 261
SequenceDescription :
Sequence

30 <213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
MGCMRWGSVL CVVVGVGASG GVLGQEFSPK LTGSATLEWG ISYGKGVGSH QAPGAVMGT 60
GPYNLKHGFR TTNVGVVSFP LVMRTTHTRR QHPALYAEI KVADLQADLS QGKAGFAVKR 120
KGKVEATLHC YGAYLTIGKN PTFLTNPALR WKPWVTAQYQ EDAVQYAPGF GGLGGKVGYS 180
35 AQDIGGSGVS LDVGFLSFAS NGAWDSTDPT HSKYGFADL KLMYARAGHP LCTVELASNV 240
TLEDGYLIGA QKDANNQNKD KLLWNVGGRL TLEPGAGFRF SFALDAGNQH QSAQDFQNR 300
QRAQSELTAL SNNLFQGESQ KQEAWVTQVV QATQTVTAG VRSALSRGT TYINALEAVQ 360
PNPAKPTGKV VQNLHTPQGS PPNLPLPAL PAFSLMGQVL LQYDAEQVVK GFEQVQTQIV 420
TEINQKVQAA VAKNNANMQA VGGSLGDTAR MVGEALIKQQ LSRKQNSILT MVSQDEVKQ 480
40 DLADLVPMR TEITAFFASV QQHITTEVKK KTDALNAGQQ IRQATQNLRA SAWRAFLMGV 540
SAVCLYLDY NVAFDALFTA QWKWLSGGYI FATAPANVFG TRVLDNTIAS CGDFAGFLKL 600
ETKSGDPYTH LTLGLDAGVE TRVYIPLTHD LYKNNNGNPL PSGGSSGHIG LPVVGKAWCS 660
YRIPVQDYGW VKPSVTVHAS TNRAHLNAPA AGGAVGATYL TKEYCAQLRA GISASLIEKT 720
VFSLDWEQGM LSDVPYLLVS ECLTQIGIRI VCGVTLWS 758
45 <212> Type : PRT
<211> Length : 758
SequenceName : SEQ ID 262
SequenceDescription :
50 Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
MGRQVMQAGV IAGMVCAASG YAGVLTQVVS GTAQLQWGIA FQKNPRTGPG KHTHGFRRTN 60
55 SLTISLPLVS KHTHTRRGEA RSGVWAQLQL KDALVELASS KSSTALSFTK PTASFQATLH 120
CYGAYLTVGT SPSCVNVFAQ LWKPFVTRAY SEKOTRYAPG FSGSGAKLGY QAHNVGNSGV 180
DVDIGFLSFL SNGAWDSTD TSKYGFADL ATLSYGVDRQ RLLTLELAGN ATLDQNYVKG 240
TEDSKNENKT ALLWGVGGRL TLEPGAGFRF SFALDAGNQH QSNAHAQTQE RAILKAREVF 300
RRVEGKLVQN LPNIMMPPGI TEQTTLIEMV GLAALIAEGT LGSATQTVLA AGALAALVSQ 360
60 LVPNIEQGVV DVFRSSDPRV VTAKLLAFLE RAPMNALNID ALLRMQWKWL SSGIYFATAG 420
TNIFGKRIFA TTRAHYFDFA GFLKLETKSG DPYTHLLTGL NAGVEARVYI PLTYIRYRN 480
GGYELNGAVP PGTINMPILG KAWCSYRIP GSHAWLAPHT SVLGTNRFN IINPAGNLLN 540
ERALQYQVGL TFSPEKVEL SAQWEQGVLA DAPYMGIAES IWSERHFGTL VCGMKVTW 598
65 <212> Type : PRT
<211> Length : 598
SequenceName : SEQ ID 263

SequenceDescription :

Sequence

5 <213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
 <400> PreSequenceString :
 MGRQVMQAGV LAGMVCAASG YAGVLTPOVS GTAQLQWGIA FQKNPRTGPG KHTHGFRRTN 60
 SLTISLPLVS KHTHTRRGEA RSGVWAQLQL KDLAELASS KSSTALSFTK PTASFQATLH 120
 10 CYGAYLTVGT SPSCVVFNAQ LWKPFVTRAY SEKDRYAPG FSGSGAKLGY QAHNVGNSGV 180
 DVIDGFLSFL SNGAWDSTDT THSKYGFAD ATLSYGVDRQ RLLTLELAGN ATLDQNYVKG 240
 TEDSKNENKT ALLWGVGGRL TLEPGAGFRF SFALDAGNQH QSNAHAQTQE RAILKAREVF 300
 RRVGKLVQN LPNIMPPGI TEQTTLIEMV GLAALIAEGT LGSATQTVLA AGALAALVSQ 360
 LVPNIEQGVV DVFSSDPRV VTAKLLAFLE RAPMNALNID ALLRMQWKWL SSGIYFATAG 420
 TNIFGKRVFA TTRAHYFDEA GFLKLETKSG DPYTHLLTGL NAGVEARVYI PLTYIRYRNN 480
 15 GGYELNGAVP PGTINMPLG KAWCSYRIPL GSHAWLAPHT SVLGTNRNFN IINPAGNLLN 540
 ERALQYQVGL TFSPEKVEL SAQWEQGVLA DAPYMGIAES IWSEHFGTL VCGMKVTW 598

<212> Type : PRT

<211> Length : 598

20 SequenceName : SEQ ID 264
 SequenceDescription :

Sequence

25 <213> OrganismName : SARS coronavirus Frankfurt 1
 <400> PreSequenceString :
 MFIFLLFLTL TSGSDDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
 PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNKN SQSVIIINNS 120
 30 TNVIRACNF ELCDNPFFAV SKPMGTQHT MIFDANFNCT FEYISDAFSL DVSEKSGNFK 180
 HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
 AQDIWGTSA AYPVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
 QTSNFRVVPV GDVVRFPNIT NLCPFGEVFN ATKFPVSVAW ERKKISNCVA DYSLVYNSTF 360
 FSTFKCYGVS ATKLNLCFS NVYADSFVVK GDDVRQIAPG QTGVADYNY KLPDDFMGCV 420
 LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCPTP ALNCYWPLND 480
 35 YGFYTTTGIG YQPYRVVLS FELNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
 SSKRFQPFQ FGRDVSDFTD SVRDPKTSEI LDISPCSFSG VSVITPGTNA SSEVAVLYQD 600
 VNCTDVSTAI HADQLTPAWR IYSTGNVVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
 HTVSLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
 NMYICGDSTE CANLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
 40 GFNFQILPD PLKPTKRSFI EDLLFNKVTI ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
 TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAAQIPF AMQMAVRFNG IGVTQNVLYE 900
 NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
 DILSRDLKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
 RVDFCGKGYH LMSFPQAAPH GVVFLHVTVV PSQERNFTTA PAICHEGKAY FPREGVVFVN 1080
 45 GTSWFITQRN FFSFQIITD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
 HTSPDVDFGD IGSINASVFN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
 GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVKGV KLHYT 1255

<212> Type : PRT

<211> Length : 1255

SequenceName : SEQ ID 265

SequenceDescription :

Sequence

55 <213> OrganismName : SARS coronavirus HSR 1
 <400> PreSequenceString :
 MFIFLLFLTL TSGSDDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
 PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNKN SQSVIIINNS 120
 60 TNVIRACNF ELCDNPFFAV SKPMGTQHT MIFDANFNCT FEYISDAFSL DVSEKSGNFK 180
 HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
 AQDIWGTSA AYPVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
 QTSNFRVVPV GDVVRFPNIT NLCPFGEVFN ATKFPVSVAW ERKKISNCVA DYSLVYNSTF 360
 FSTFKCYGVS ATKLNLCFS NVYADSFVVK GDDVRQIAPG QTGVADYNY KLPDDFMGCV 420
 65 LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCPTP ALNCYWPLND 480
 YGFYTTTGIG YQPYRVVLS FELNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
 SSKRFQPFQ FGRDVSDFTD SVRDPKTSEI LDISPCSFSG VSVITPGTNA SSEVAVLYQD 600

VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSSIAYS NNTTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLQLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQLLPD PLKPTKRSFI EDLLFNKVTI ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
5 TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRDLKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVVFVN 1080
GTSWFITQRN FFSFQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
10 HTSPDVLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEY YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
15 SequenceName : SEQ ID 266
SequenceDescription :

Sequence

20 <213> OrganismName : SARS coronavirus ZJ01
<400> PreSequenceString :
MFIFLLFLTL TSGSDDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
TNVVIRACNF ELCNDPFFAV SKPMGTQHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
25 HLREFVFKNK DGFLYVYKGY QPIDVVRDL P SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSA AAYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPV GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNVNYKY RYL RHGKLRP FERDISNVFP SPDGKPCPTP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
30 SSKRFQPFQ FGRDVSDFD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSSIAYS NNTTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLQLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
35 GFNFSQLLPD PLKPTKRSFI EDLLFNKVTI ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRDLKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVVFVN 1080
40 GTSWFITQRN FFSFQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEY YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVKGV KLHYT 1255

<212> Type : PRT
45 <211> Length : 1255
SequenceName : SEQ ID 267
SequenceDescription :

Sequence

50 <213> OrganismName : SARS coronavirus TW1
<400> PreSequenceString :
MFIFLLFLTL TSGSDDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
55 TNVVIRACNF ELCNDPFFAV SKPMGTQHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDL P SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSA AAYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPV GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
60 LAWNTRNIDA TSTGNVNYKY RYL RHGKLRP FERDISNVFP SPDGKPCPTP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQ FGRDVSDFD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSSIAYS NNTTIAIPTNF SISITTEVMP VSMAKTSVDC 720
65 NMYICGDSTE CANLLQLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQLLPD PLKPTKRSFI EDLLFNKVTI ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900

NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
 DILSRDLKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
 RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVVFVN 1080
 GTSWFTTQRN FSPQIIITD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
 5 HTSPDVLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
 GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCKKFDE DDSEPVKGV KLHYT 1255

<212> Type : PRT
 <211> Length : 1255
 10 SequenceName : SEQ ID 268
 SequenceDescription :

Sequence

15 <213> OrganismName : SARS coronavirus CUHK-Su10
 <400> PreSequenceString :

MFIFLLFLTL TSGSDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
 PFYSNVTFGH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
 TNVVIRACNF ELCNDPFFAV SKPMGTQHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
 20 HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
 AQDIWGTSA AYPVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
 QTSNFRVVPV GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
 FSTFKCYGVS ATKLNLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
 LAWNTRNIDA TSTGNYNKY RYLRHGKLRP FERDISNVPF SPDGKPCPTP ALNCYWPLND 480
 25 YGFYTTTGIG YQPYRVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLT 540
 SSKRFQPFQ FGRDVSDFTD SVRDPKTSEI LDISPCSFEG VSVITPGTNA SSEVAVLYQD 600
 VNCTDVSTAI HADQLTPAWR IYSTGNVVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
 HTVSLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
 NMYICGDSTE CANLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
 30 GFNFQILPD PLKPTKRSFI EDLLFNKVTI ADAGFMKQYG ECLGDINARD LICAQKFNG 840
 TVLPPLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
 NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
 DILSRDLKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
 RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVVFVN 1080
 35 GTSWFTTQRN FSPQIIITD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
 HTSPDVLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
 GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCKKFDE DDSEPVKGV KLHYT 1255

<212> Type : PRT
 40 <211> Length : 1255
 SequenceName : SEQ ID 269
 SequenceDescription :

Sequence

45 <213> OrganismName : SARS coronavirus Urbani
 <400> PreSequenceString :

MFIFLLFLTL TSGSDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
 PFYSNVTFGH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
 50 TNVVIRACNF ELCNDPFFAV SKPMGTQHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
 HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
 AQDIWGTSA AYPVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
 QTSNFRVVPV GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
 FSTFKCYGVS ATKLNLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
 55 LAWNTRNIDA TSTGNYNKY RYLRHGKLRP FERDISNVPF SPDGKPCPTP ALNCYWPLND 480
 YGFYTTTGIG YQPYRVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLT 540
 SSKRFQPFQ FGRDVSDFTD SVRDPKTSEI LDISPCSFEG VSVITPGTNA SSEVAVLYQD 600
 VNCTDVSTAI HADQLTPAWR IYSTGNVVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
 HTVSLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
 60 NMYICGDSTE CANLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
 GFNFQILPD PLKPTKRSFI EDLLFNKVTI ADAGFMKQYG ECLGDINARD LICAQKFNG 840
 TVLPPLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
 NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
 DILSRDLKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
 RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVVFVN 1080
 65 GTSWFTTQRN FSPQIIITD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
 HTSPDVLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200

GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
5 SequenceName : SEQ ID 270
 SequenceDescription :

Sequence

10 <213> OrganismName : SARS coronavirus
 <400> PreSequenceString :
MFIFLLFLTL TSGSDLDRC TFDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
PFYSNVTFGH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
TNVVIRACNF ELCDNPFFAV SKPMGTQHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
15 HLREFVFNK DGFLYVYKGY QPIDVVRDL SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVP GDVVRFPNIT NLCPFGEVFN ATKFPVSYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNLCFS NVYADSFVVK GDDVRQIAPG QTGVADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCPP ALNCYWPLND 480
20 YGFYTTTGIG YQPYRVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQ FGRDVSDFTD SVRDPKTSEI LDISPCAFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
25 GFNFSQLPD PLKPTKRSFI EDLLFNKVTI ADAGFMKQYG ECLGDINARD LICAQKFNG 840
TVLPPLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NOKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRDLKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
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30 GTSWFITQRN FSPQIITTD NTFVSGNCV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVLGD ISGINASVNN IQKEIDRLNE VAKNLNESLI DLQELGKYEY YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
35 <211> Length : 1255
 SequenceName : SEQ ID 271
 SequenceDescription :

Sequence

40 <213> OrganismName : SARS coronavirus Tor2
 <400> PreSequenceString :
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PFYSNVTFGH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
45 TNVVIRACNF ELCDNPFFAV SKPMGTQHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFNK DGFLYVYKGY QPIDVVRDL SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVP GDVVRFPNIT NLCPFGEVFN ATKFPVSYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNLCFS NVYADSFVVK GDDVRQIAPG QTGVADYNY KLPDDFMGCV 420
50 LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQ FGRDVSDFTD SVRDPKTSEI LDISPCAFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
55 NMYICGDSTE CANLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQLPD PLKPTKRSFI EDLLFNKVTI ADAGFMKQYG ECLGDINARD LICAQKFNG 840
TVLPPLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NOKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRDLKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVVFVN 1080
60 GTSWFITQRN FSPQIITTD NTFVSGNCV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVLGD ISGINASVNN IQKEIDRLNE VAKNLNESLI DLQELGKYEY YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

65 <212> Type : PRT
 <211> Length : 1255
 SequenceName : SEQ ID 272

SequenceDescription :

Sequence

5 <213> OrganismName : SARS coronavirus GD01
 <400> PreSequenceString :
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 TNVIVIRACNF ELCDNPPFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
 10 HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFLP 240
 AQDTWGTSA AAYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
 QTSNFRVVPV RDVVRFPNIT NLCPFGEVFN ATKFPVSVAW ERKRISNCVA DYSLVYNSTF 360
 FSTFKCYGVS ATKLNLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
 LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCPP ALNCYWPLND 480
 15 YGFYTTTGIG YQPYRVVVLV YELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
 VNCTDVSTAI HADQLTPAW IYSTGNVVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 600
 HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
 NMYICGDSTE CANLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKDFG 780
 20 GFNFSQILPD PLKSTKRSFI EDLLFNKVTI ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
 TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTONVLYE 900
 NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
 DILSRDLKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
 RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVVFVN 1080
 25 GTSWFITQRN FFSPPQIITD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
 HTSPDVLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEY YIKWPWYVWL 1200
 GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCKCFDE DDSEPVKGV KLHYT 1255

<212> Type : PRT

30 <211> Length : 1255

SequenceName : SEQ ID 273

SequenceDescription :

Sequence

35 <213> OrganismName : SARS coronavirus CUHK-W1
 <400> PreSequenceString :
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 PFYSNVITGFH TINHTFDNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
 40 TNVIVIRACNF ELCDNPPFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
 HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
 AQDTWGTSA AAYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
 QTSNFRVVPV GDVVRFPNIT NLCPFGEVFN ATKFPVSVAW ERKKISNCVA DYSLVYNSTF 360
 FSTFKCYGVS ATKLNLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
 45 LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCPP ALNCYWPLND 480
 YGFYTTTGIG YQPYRVVVLV FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
 SSKRFQPFQ FGRDVSDFTD SVRDPKTSEI LDISPCSFSG VSVITPGTNA SSEVAVLYQD 600
 VNCTDVSTAI HADQLTPAW IYSTGNVVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
 HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
 50 NMYICGDSTE CANLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKDFG 780
 GFNFSQILPD PLKPTKRSFI EDLLFNKVTI ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
 TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTONVLYE 900
 NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
 DILSRDLKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
 55 RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVVFVN 1080
 GTSWFITQRN FFSPPQIITD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
 HTSPDVLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEY YIKWPWYVWL 1200
 GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCKCFDE DDSEPVKGV KLHYT 1255

60 <212> Type : PRT

<211> Length : 1255

SequenceName : SEQ ID 274

SequenceDescription :

65 Sequence

<213> OrganismName : SARS coronavirus BJ01

<400> PreSequenceString :
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TNVIRACNF ELCDNPPFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
5 HLERFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDTWGTSA A YFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPV GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSLVLYNSTF 360
FSTPKCYGVS ATKLNLCFVS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNKY RYLRHGKLRP FERDISNVFF SPDGKPCPP ALNCYWPLND 480
10 YGFTTTTIG YQPYRVVLS FELNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLT 540
SSKRFQPFQ FGRDVSDFTD SVRDPKTSEI LDISPCSFSG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
15 GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNG 840
TVLPLLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRDLKVE AEFVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFHVTVYV PSQERNFTTA PAICHEGKAY FPREGVVFVN 1080
20 GTSWFITQRN FFSPQIITD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKEYFKN 1140
HTSPDVLGD ISGINAVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEY YIKWPWYVWL 1200
GFIAGLIAIV MTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVKGV KLHYT 1255

<212> Type : PRT
25 <211> Length : 1255
SequenceName : SEQ ID 275
SequenceDescription :
Sequence

30 <213> OrganismName : SARS coronavirus
<400> PreSequenceString :
SGFRKMAFPS GKVEGCMVQV TCGTTTLNGL WLDDTVYCPH HVICTAEDML NPNYEDLLIR 60
KSNHSFLVQA GNVQLRVIGH SMQNCLLRK VDTSNPKTPK YKQVRIQPGQ TFSVLACYNG 120
35 SPSGVYQCAM RPNHTIKGSF LNGSCGSGVF NIDYDCVSFC YMHMELPTG VHAGTDLEGK 180
FYGPVDRQT AQAAGTDTTI TLNVLAWLYA AVINGDRWFL NRFTTTLNDF NLVAMKYNIE 240
PLTQDHVDIL GPLSAQTGIA VLDMCAALKE LLQNGMNGRT ILGSTILEDE FTPFDVVRQC 300
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<212> Type : PRT
40 <211> Length : 306
SequenceName : SEQ ID 276
SequenceDescription :
Sequence

45 <213> OrganismName : SARS coronavirus
<400> PreSequenceString :
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KMADQAMTQM YQARSEDKR AKVTSAMQTM LFTMLRKLND DALNNIINNA RDGCVPLNII 120
50 PLTTAAKLMV VVPDYGTYN TCDGNTFTYA SALWEIQQV DADSKIVQLS EINMDNSPNL 180
AWPLIVTALR ANSAVKLQ 198
<212> Type : PRT
<211> Length : 198
SequenceName : SEQ ID 277
55 SequenceDescription :
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60 <213> OrganismName : SARS coronavirus
<400> PreSequenceString :
AGNATEVPAN STVLSFCAFA VDPKAYKDY LASGGQIPIT CVKMLCTHTG TGQAITVTE 60
ANMDQESFGG ASCCLYCRCH IDHPNPKGFC DLKGYVQIP TTCANDPVGF TLRNTVCTVC 120
GMWKGYGCSG DQLREPLMQ 139
<212> Type : PRT
65 <211> Length : 139
SequenceName : SEQ ID 278
SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus
5 <400> PreSequenceString :
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GTGTIYTELE PPCRFVTDTP KGPVKVLYLF IKGLNNLNRG MVLGSLAATV RLQ 113

<212> Type : PRT
10 <211> Length : 113
SequenceName : SEQ ID 279
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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SMAFGVSAIS EGDRSIALGA SSYSLGQYSM ALGRYSKALG KLSIAMGDSS KAEGANAIAL 180
GNATKATEIM SIALGDTANA SKAYSMALGA SSVASEENAI AIGAETEAAE NATAIIGNNAK 240
AKGTNSMAMG FGSLADKVNT IALNGSQAL ADNIAIGQG NKADGVDAIA LGNGSQSRGL 300
NTIALGTASN ATGDKSLALG SNSSANGINS VALGADSIAD LDNTVSVGNS SLKRKIVNVK 360
25 NGAIKSDSYD AINGSQLYAI SDSVAKRLGG GAAVDVDDGT VTAPTYNLKN GSKNNVGAAL 420
AVLDENTLQW DQTKGKYSAA HGTSSPTASV ITDVADGTIS ASSKDAVNGS QLKATNDDVE 480
ANTANIAINT SNIATNTANI ATNTNTITNL TDSVGLQAD ALLWNETKKA FSAAHGQDIT 540
SKITNVKAD LTADSTDAVN GSQKKTNDNA VATNTNIN NTSNIATNTT NISNLTETVT 600
NLGEDALKWD KDNQVFTAAH GTETTSKITN VKDGLTTGS TDAVNGSQLK TTNDAVATNT 660
30 TNIAITNTNI SNLTETVTNL GEDALKWDK NGVFTAAHGN NTASKITNIL DGTVTATSSD 720
AINGSQLYDL SSNIATYFGG NASVNTDGVF TGPTYKIGET NYYNVGDALA AINSSFSTSL 780
GDALLWDATA GKFSAKHGTN GDASVITDVA DGEISDSSSD AVNGSQLHGV SSVVVDALGG 840
GAEVNADGTI TAPTYTIANA DYDNVGDALN AIDTTLDDAL LWDADAGENG AFSAAHGKDK 900
TASVITNVAN GAISAASSDA INGSQLYTTN KYIADALGGD AEVNADGTIT APTYTIANAE 960
35 YNNVGDALDA LDDNALLWDE TANGGAGAYN ASHDGKASII TNVANGSISE DSTDAVNGSQ 1020
LNATNMIEQ NTQIINQLAG NTDATYIQEN GAGINYVRTN DDGLAFNDAS AQGVGATAIG 1080
YNSVAKGDSS VAIGQGSYSD VDTGIALGSS SVSSRYIAKG SRDTSITENG VVIGYDITDG 1140
ELLGALSTGD DGKYRQIINV ADGSEAHDAV TVRQLQNAIG AVATTPTKYF HANSTEEDSL 1200
AVGTDLSLNG AKTIVNGDKG IGIGYGAYVD ANALNGIAIG SNAQVIHVNS IAINNGSTTT 1260
40 RGAQNTYAY NMDAPQNSVG EFSVGSADGQ RQITNVAAGS ADTDAVNNGQ LKVTDAQVSQ 1320
NTQISITLND RVTNLDNRVT NIENGLDIV TTRGSKYFKT NTDGVDASQ GKDSVAIGSG 1380
STAAADNSVA LGTGSVATEE TTISVGSSTN QRRITNVAAG KNATDAVNVA QLKSSSEAGGV 1440
RYDTKADGSI DYSNITLGGG NGGTTRISNV SAGVNNNDVV NYAQLKQSVQ ETKQYTDQRM 1500
VEMDNKLSKT ESKLSGGIAS AMAMTGLPQA YTPGASMASI GGGTYNGESA VALGVSMVSA 1560
45 NGRWVYKLQG STNSQGEYSA ALGAGIQW 1588
<212> Type : PRT
<211> Length : 1588
SequenceName : SEQ ID 280
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
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TNGVGNTGSG SRDITIDANL PGLRVDTVAG DDVNSIEHA QALVITGSSS GLAAGAALT 180
VINTVTYAAT VLADGTWSVG VPAADVSNWP AGTVNITVSG TNTAGTTSTI THPVTVDLAA 240
VAISINTVSG DDVINAAEKG ADLTLGSGTS GVEVGQTVTV TFGGKTYTAT VAGDGSWTTT 300
60 VPAADLSVLR DGDATVQASV STINGTASA THAYSVDATA PTLAINTIAT DDILNAAEAG 360
NPLTISGSST AEAGQTVTVT LNGVTYSGSV QADGSWSVSL PTADLSNLTA SQYTVSASVS 420
DKAGNPASAN HGLAVDLTVP VLTINTVSGD DIINAEEHGQ ALVISGSSTG GEAGDVITVT 480
LNSKTYTTML DASGNWSVG VPAADVTLGS GPQTITAAIT DAAGNSDDAS RTVTVNLAAP 540
TIGINTIATD DVIKATEKGA DLQITGTSNQ PAGTTTIVTL NGQNYTATTD SNGNWSATVP 600
65 ASAVSALGEA NYTVTANVTD TAGNSNSASH NVLVNSALPA VTINAVATDD IINAESGNA 660
QTISGQVGA AQGDTVTVTL GGNTYTATVQ SNLSWSVDVP AADIQALNG DLTVNASVTN 720
GVGNTGSGSR DITIDANLPG LRVDTVAGDD VINSIEHNQA LVITGSSSGL TAGTALTVEI 780

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	ITINTLSGDD	VINAVEKGET	LUVSGSTSGV	EAGQTVTVTF	GGKNYTTTVE	ANGSWTVNV	900
	PADLAALPDG	AGNVQASVSN	INGNSAQADR	AYSVDATAPL	VTINTIASDD	ILNVSEAGAG	960
	ITISGTTTAAQ	AGQTLTVTLN	NNTYQTTVLA	DGTWSVNVPA	ADLSGLTASS	YTVTATVSDK	1020
5	AGNPASADHA	LVVDITAPDL	TINTVAGDDI	INAIEHGQAL	VVSGTSTGAA	AGDVVTVTLN	1080
	GKNYTTTLDA	SGNWSVGIPA	ADVTALATGS	QTTTASLSDR	AGNSDSTHSD	VTYDLSGPTL	1140
	TINTVSGDDI	INAAEIVVAQ	TISGQVTGTA	VAGNTVIVTI	GGNQYNATVQ	SDLWSVSVSP	1200
	ANVLQALNGG	ELTISASLTN	SANNTGTATH	DIVIDANLPG	LRVDTVAGDD	VINSIEHTQA	1260
	LVITGSSSSL	AAGAALTUVI	NSVTYGATVL	ADGWSVSGVP	VADVTNWPAG	TVNIAVSGTN	1320
10	TAGTTTISH	PVTVDLAAVA	ITINTLSTDD	VINAEEKGSD	LQLSGTTSKV	EAGQTTITVF	1380
	GGKSYTTTVA	ADNTWGLTIP	AVDVATLPDG	AANVQASVSN	VAGNSTQATH	AYSVDATAPS	1440
	VTINTIATDD	ILNAAEAGSA	LTISGTSTAE	AGQTVTVTLN	GVNYSQNVQA	DGSWSVSVPT	1500
	GDLASLTASS	YTVNASVSDK	ARNASASATHN	LTVDLAAPVV	TINTVAGDDI	INATEHGQAQ	1560
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15	AGNSGTASHT	VTVALGAPVL	AINITIAVDDI	INAAEKGADL	AITGTSNQPA	GTQITVTLNG	1680
	QNYTTTADAS	GNNVSVTPAS	RVSALGEATY	TVTAAATDAD	GNSGSASHNV	QVNTALPGVT	1740
	INVVATDDII	NAAEAGVEQT	ISGQVTGAAA	GDTVTVTLGG	ATYTATVQAN	LSWSVDVPAS	1800
	ALQELGNGEL	TISASVTNSV	GNTGNGTREI	TIDANLPLGR	VDTVAGDDVV	NIEHGQALV	1860
	ITGSSSSGLAA	GSNVTLTING	QTYVAAVLAD	GTWSVGVPV	DVSAWPAGSV	TIAASGSTSA	1920
20	GNPVSVTHPV	TVDLASAVVS	INAITADDVI	NAAEKGAAIT	LSGSTSGVEA	GQTVTVTFGG	1980
	KTVSATVAAN	GSWSTVPA	DMAALRDGDA	SAQASVSNVN	GNSATTTHAY	SVDASAPT	2040
	INTIAGDIL	NAAEAGAAIT	ITGSSSTAEAG	QTVTVTLNGT	NYTGTVTQDG	SWSVSVPSAD	2100
	LSTLTASNYT	VNAASVSKAG	NPASVNHMLT	VDTSVPVVTI	NTVAGDDVIN	ATEHAQAQII	2160
	SGSATGAATG	STVTVTIGTN	TFTTVLDASG	NWSVGVPASV	VSALANGTVT	INASVTDAGG	2220
25	NSGSATHQVT	VNTGLPTITF	NAISGDNILN	ADEKGQPLTI	SGGSTGLATG	AQVTVTLNGH	2280
	NYSATTDSAG	NGLTVPVSD	LAALGQANYT	VSASATSAAG	NTASSQANLL	VDSGLPDVTI	2340
	NTVAGDDIIN	AAEAGADQTI	SGVVTRAAG	DTVTVTLLGN	TYTATVQSNL	SWSVSVPTAD	2400
	LQALGNGDIT	ITASVTNANG	NTGSGTRDIT	IDANLPLGRV	DTVAGDDIVN	SIEHGQALVI	2460
	TGSSSGLNAG	AVLTVTINSV	AYSATVQADG	SWSVGIPAA	VSAPAGPLT	VEVDGQSSAN	2520
30	NPVSVSHPT	VDLTAVAI	NTVASDDVIN	NAEKGTLNLT	SGSTSGIESG	QTVTVTFGGK	2580
	TYTASVAANG	SWSVNVPAAD	LATLPEGAAN	VQASVSSASG	NSASATHAYS	VDASAPTLTI	2640
	NTIASDDILN	AAEAGSPLTI	SGTSTAETGQ	TVTVTLNGAT	YTGTVQADGS	WSVSVPTSAL	2700
	GALNASNTTV	SATVNDKAGN	PGSASHNLAV	DTTAPVLTIN	TVAGDDIIND	AEHAQALVIS	2760
	GTSSSGEAGD	VVSVVLNGKT	YTTTLDASGN	WSVGVPAAV	TALGSGAQTI	TASVSDRAGN	2820
35	SDDASRTVTV	SLAPVISIN	TIAGDDVINA	TEKSGDLALS	GTSDQPAQTA	ITVTLNGQNY	2880
	SATTTDASGNW	SVTVPASAVS	ALGEATYSVT	ASVINAQGNS	STASHNVQVN	TALPGITINP	2940
	VATDDIINAS	EAGSAQTISG	QVTGAAAGST	TVTLGCKTY	TATVQADLSW	NVSVPAAWDQ	3000
	ALNGELTVN	ASVTNAVNGT	SGSTRDITD	ASLPLGRVDT	VAGDDVNNII	EHAQAQVITG	3060
	SSSGFAAGTA	LTVVINNQTY	AATVLANGSW	SVGPATDVS	NWPAGTLNIT	VSGANSAGTQ	3120
40	TSITHPLTVD	LTAVAISMNS	ITSDDAINAA	EKGAAITLGS	STSGVEAGQT	VTVTFGGKTY	3180
	TTTVAANGSW	STTVPAADLA	ALRDGDASAQ	VRVTNVNGNS	ATATHEYSVD	SAAPT	3240
	IASDNIINAS	EAAAGVTVSG	TSTAQTGQTL	TVTLNGTNYQ	TTVQTDGWS	LTLPASDLTA	3300
	LANNGYTLTA	TVSDLAGNLG	SASKGVTVD	TAPVISFNTV	AGDDVINNV	HIQAQIISGT	3360
	ATGAVAGDRL	VVTIAGQQYV	TSTDASGNWS	VGVPASVISG	LADGTVTISA	TITDSAGNSS	3420
45	TQTHNVQNT	AAVSLSVSTI	SGDNLINAAE	AGSALTLSGT	GTNFATGTVV	TVLLNGKGY	3480
	ATIQNGSWS	VNVPAADVAA	LSDGTSYTVS	ASAQDSAGNG	NSSTQTHNVQ	VNTAAVSLSV	3540
	STISGDNLIN	AAEAGSALT	SGTGTNFATG	TVTVLLNGK	GYSATIQSNG	SWSVNVPAAD	3600
	VAALSDGTSY	TVSASAQDSA	GNSATASRSV	AVDLTAPVIS	INTVSTDDRL	NAAEQQPLT	3660
	LNGSTSAEVG	QTVTVTFGGK	TYTATVAANG	TWALNVPAD	LAALGQGAQT	ITASVNDRAG	3720
50	NPGQATHALT	VDTVAPT	ATVAGDDIIN	NAEQLAGQTI	SGTTTAEVQ	TVTVTFNGQT	3780
	WSATVSGSGS	WSVFIPAQQF	AGLSGGSYTI	SATVSDQAGN	PGSASRGVTL	NGDVPTVTIN	3840
	TFAGDDVVNA	AEHGSSLVIS	GTTTAPVGQT	LTLTLNGKTY	TTTVQTGGSW	SYTLGSADVT	3900
	ALADGNAYVI	NASVSNAGN	TGSSNHTITV	DLSAPAMGIN	IDSLQADTGL	SASDFITSVS	3960
	PVVVNGSLTA	ALASNETAQI	SIDGGTTWTT	LTVTGTWRY	NDSRTLTDGN	YLYQVRVIDA	4020
55	AGNVGATDSQ	NVVIDTTAPD	PAVKTIAISA	ITTDMLITN	DFVTSDTTLA	VSGTLGATLS	4080
	AGEFAQISLD	GGVTWTTLT	VGTSSWYADG	HTLTDGTWNY	TVRVVDLAGN	VGQTATQNVV	4140
	VDTTSPAAK	SITITGISDD	TGTSSSDFIT	SDTTLTVRGV	LGAALGANEF	AQISTDNGAT	4200
	WVNVTVAAAS	LNWSYVDGRT	LTNGTTTWQV	RVVDLAGNVG	ATSSQSALID	TVNPAQVLT	4260
	ASISTDTGSS	ATDFITSMT	LTLTGSLGAG	LASGEVAQIS	LDGATWTTL	TTNGTQWY	4320
60	DSRTLTGDSY	VYQVRVLDLA	GNTGPVVSKT	VVVDINPTA	TPTIVSYTDD	VGQRQGLTSS	4380
	SQATDDTTP	LNGVLSAPLA	SCEVVYLYRN	GLLLGAVTMV	GALNWTYSDS	GLVSGAYTYS	4440
	ARVVDLAGNI	TSSSDFVLT	DTSIPTTLAQ	ITSQTRDIT	PIISGVITAA	LASGQYVEV	4500
	INGKTYTSEP	GGAVVVDPAH	NTWYVQLPDT	DALTVSATAY	TVTAQVKSSA	GNGNNANISN	4560
	GTVTVNAID	YTPTWTTASK	TTAWGLTYGL	DSHGMMTVLA	NQQVMQSTDP	LTWSKTALTL	4620
65	YQSGNNYATS	SIADYDRNGT	GDLFITRDDY	GTGYINGFTN	NGDGTFS	QVTVGLT	4680
	GSIVAFDKEG	DGVLDFWIGD	AGGPDSTNFT	WNNAGTLVGN	STTSNNGGSA	TVGGAVTGXL	4740
	SLNEGSGVDL	NNDGRIDLQV	HTYNLNNYYT	LSSLINQNG	TFVWQNTTN	TFLSGAGSGA	4800

MSSSVSMTWA DFDGDGMDL FLPASQGRAN YGSLLENTNG VLGPVAVGA TATTYASQFS 4860
LAVDWNHDL MDIARIAQTG QSYLYTNVSN ASNWTQSALG GSQSGTTSKV AAMDYDWDGA 4920
VDVLVSKQSG SVFLSRNTNT VSYGTSLSHLR ITDPNGINVT YGNTVVKLYNS AGVLVATQII 4980
NPQSGMGVND TSALVNFYGL NAGETYNVAVL IKSTGTASN IDQTVNTSWG GLQATDATHA 5040
5 YDLSAEAGTA SNNGKFPVGTG YNDTFFATAG TDTYDGSQGW VYSSGTGTWL ANGGMDVVDV 5100
RLSTVGV TAN LSSTAQAATG FNTSTFTNIE GISGSNFNDI LTGSSGDNQL EGRGGNDTLN 5160
IGNGGHDTLL YKLLNASDAT GGNGSDVVG FTVGTWEGTA DTDRIDIREL LQSGGYTGNG 5220
KASYVNGVAT LDAQAGNIGD FVKVTQSGSD TIVQIDRDGT GGTATTNVV TLTGVHTDLA 5280
TLLANHQLMV V 5291

10 <212> Type : PRT
<211> Length : 5291
SequenceName : SEQ ID 281
SequenceDescription :

15 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MGVHTAEATL PNGNNDTKIV NIAPDASNAQ VTLNIPAAQV VTNNSDSVQL TATVKDPSNH 60
20 PVAGITVNF MPQDVAANFT LENNGIAITQ ANGEAHVTLK GKKAGTHTVT ATLSNNNTSD 120
SQPVTFVADK TSALVVLQIS KNEITGNGVD SATLTATVKD QFDNEVNLP VTFSTASSGL 180
TLTPGESNTN ESGIAQATLA GVAFGEQTVT ASLANNGASD NKTVHFIGDT AAKIIELTP 240
VPDSIIAGTP QNSSGSGVITA TVVDNNGFPV KGVTVNFTSN AATAEMTNGG QAVTNEQGKA 300
TVTYTNRSS IESGARPDVT EASLENGSST LSTSINVNAD ASTAHLTLLQ ALFDTVSAGD 360
25 TTNLVIEVD NYNGVVPQOE VTLVSPSEG VTPSNNAIYT TNHDGNFYAS FTATKAGVYQ 420
VTATLENGDS MQQTVTYVPN VANAEISLAA SKDPVIANN DLTLTATVA DTEGNAIANS 480
EVTFTLPEV RANFTLGDG KVVTDTEGKA KVTLLKGTAG AHTVTASMAK GKSEQLVNVF 540
IADTLTAQVN LNVTEDNFIA NNVGMLRLQA TVTDGNGNPL ANEAVTFTLP ADVSASFTLG 600
QGSAGITDIN GKAEVTLSGT KSGTYPVTVS VNNYGVSDTK QVTLIADAGT AKLASLTSVY 660
30 SFVVTTEGA TMTASVTDAN GNPVEGIKVN FRGTSVTLSS TSVETDDRGF AEILVTSTEV 720
GLKTVSASLA DKPTEVISRL LNAKADINSA TITSLEIPEG QMVAAQDVAV KAHVNDQFGN 780
PILNESVTFE AEPPEHMTIS QNVSTDTTHG IAEVTMTPER NGSYMVKASL ANGSSYEKDL 840
VVLDQKLTL ASSPLIGVNS PTGATLTATL TSANGTPVEG QVINFSVTPE GATLSGGKVR 900
TNSSGQAPVV LTSNKVGTYT VTASFHNGVT IQTQITVKVT GNSSTAHVAS FIADPSTIAA 960
35 TNSDLSTLKA TVEDGSGNLI EGLTVYFALK SGSATLTSLT AVTDQNGIAT TSVRGAITGS 1020
VTVAVTTAG GMQTVDTILV AGPADASQSV LKNRSSLKGF DFTDSAEHL VLHDISGNPI 1080
KVSEGLEFVS SGTNAPVQV SAIDYSKNFS GEYKATVTGG GEGIATLIPV LNGVHQAGLS 1140
TTIQFTRAED KIMSGTVLVN GANLPTTTFF SQGFTGAYYQ LNNDNFAPGK TAADYEFSSS 1200
ASWVDVDTG KVTFTKVGSK WERITATPKT GGPSYIYER VKSWVWVAGD AFMIYSLAEN 1260
40 FCSSNGYTLF LGDHLNHSRS RGIGSLYSEW GDMGHYTEA GFHSNMYWSS SPANSNEQYV 1320
VSLATGDQSV FEKLGAYAT CYKNL 1345
<212> Type : PRT
<211> Length : 1345
SequenceName : SEQ ID 282
SequenceDescription :

45 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSLIIDVISR KTSVKQTLIN PGDVTVVIYE PSVQVHAQA SAVARYVREG NDLLIYMQDG 60
50 TVIRCNGYFL QAANTAEQSE LVFADGQQLT HITFADTAAG GLAPVELTAQ TTAIESIAPF 120
LDTVAQTSFA PWGWLGAAGV GGGALGALLA SGGDGSKTE VINNPTPPAE PGNATPSFLV 180
TDNQGDQGI LATNDITDDT TPTFSGSGQA GATIQIKDSN GNTIASTQVD NNGHWSVSLP 240
55 TQSAGEHTWS VVQIVGSTIT DAGSITLTID NSQASQVAT TAGDNIINAS EQAAGFTLSG 300
TSSHLAQTE LTVTLNGKTY TTSVGANGAW SVQVPTADAQ ALGEGNQAVL VSGKDATGNT 360
VTGAQLLTV TQPTLAIN IAQDNIIASA EHNVALVLSG TSNAEAGQTV TLTVNGKSH 420
ATVSGDGTWQ VTLPADEVQA LAEGNYAVNA SVSDRAGNTT SHSANFTVDT SAPVVSNTV 480
AGDDILNNAE QAVAQIISGQ VSGASPGDTV TVKLGTHTVLT GIVLADGSWN VALDPAVTRT 540
60 LDRGANTIFV TVTDAAGNTG AASRAITLVG VSPLITINTV SGDDIISGAE KGAPLTLTG 600
TQQAETGQTV TVTLAQGSFT TTVQADGSWS LTVPAAAMGN LPPDGAVAITA SVTDLSGNTG 660
NTSRITIVDS QAPALSIDPL TADNIIAAE SGQDLPTGT TDAQPGQTV VTLNGQTYQG 720
VVQPDGTWSV TVPAANVGAL ADGNATVTAS VNDVAGNPSS VSRVALVDAT PPVVTINPVA 780
TDNVINTPEH AQAQIISGTV TGAQAGDIVT VTLNNVDYTT VVDGSGNWSL GVPASVVSGL 840
65 ADGSPVSVS VTDKAGNTGS QSLTIVTVNS APLIGINSIA GDDVINASEK GADLQITGTS 900
DQPVNTAITV TDSAGNWSVT VPASAVTALG QANYTVTAAV TSDIGNSATA 960
SHNVLVDSAL PGVTINPVAT DDIINAAEAG VAQTISGQVT GAEDGDTVTT TLGGNTYTAT 1020

VGSNLTWSVD VPAADIQALG NGDLTVNASV TNQNGNTGSG TRDITIDANL PGLRVDTVAG 1080
DDVNIIEHG QALVVTGSSS GLAESTPLTV TINNVEYTTA VQADGSWSVG VTAAQVSAWP 1140
AGTVNIAVSG ESSAGNSVSI THPVTVDLTP AAITINTIAT DDVINAEEKG ADLTLSTGTTT 1200
NVEPGQTVTV TFGGKNYAS VASDGSWTAT VPAADLASLP EGSASALASV SNINGNSASA 1260
5 VHNYSVDSSA PTIIINTVAS DNIIVNASEAD AGVTVSGSTT AEAGQIVTIT LNSPTVQTYQ 1320
ATVQADGSWS INIPAADLEA LTDGSHTLTA TVNDKAGNPA STTHNLAVDL TVPVLTTINTI 1380
AGDDIINATE HGQALVISGS STGGEAGDVV TVTLNSKTYT TTLDASGNWS VGVPAADVTA 1440
LGSGPQTVTA TVTDAAGNSD N 1461
<212> Type : PRT
10 <211> Length : 1461
SequenceName : SEQ ID 283
SequenceDescription :

Sequence

15 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNRIYRVWNL CTLQVFQACS ELTRRVGKTS TVNLRKSSGL TTKFSRLTLG VLLALSGSVS 60
GASLEVDNGQ ITNIDTDVAY DAYLVGWYGT GVLNLAGGN ASLTITTSV IGGNEDSEGT 120
20 VNVLGGTWRL YDSGNARPL NVGQSGTGTL NIKQKGHVDG GYLRLGTQAA GVGTVNVEGE 180
DSVLTTLEFE IGSYGTGSLN ITDKGYVTSS IVAILGYQAN SNGKVVEKG GEWLKNNDS 240
SIEFQIGNQG TGEATIREGG LITAENTIIG GNATGVGTLN VQDQDSVITV RRLYNGYFGN 300
GAVNISNNGI INNKEYSLVG VQDGSBGVVN VTDKGHWNFL GTGEAFRIY IGDAGDGELN 360
VSREGKVDSD IITAGMKETG TGNLTVKDKN SVITNLGTNL GYDGHGEMNI SNEGLVVSNG 420
25 GSSLGYGETG VGKVSITGG IWEVKNVYIT TIGVAGVGNL NISDGGKFVS QNITFLGDKA 480
SGIGTLNLM D ATSSFDTVGI NVGNFGSGIV NVSNGATLNS TGYGFIGGNA SGKGIVNIST 540
DSLWNLKTSS TNAQLLQVGV LGTGELNITT GGIVKARDTQ IALNDKSKGD VRVDGQNSLL 600
ETFNMYVGTG GTGTLLTINS GTLNVEGGEV YLGVFEPAVG TLNIGAAHGE AAADAGFITN 660
ATKVEFGSGE GVFFVFNHTN SDAGYQVDM ITGDDKDGKV IHDAGHTVFN AGNTYSGKTL 720
30 VNDGLLTIAS HTADGVTGMG SSEVTIASPG TLDILASTNS AGDYTLTNAL KGDGLMRVQL 780
SSSDKMFQFT HATGTEFAGV AQLKDSFTTL ERDNTAALTH AMLQSDIENT TSVNVGEQSI 840
GGLAMNGGTL IFDITDIPAA LAEGYISVDI LVVGASDVTW KGRNYQVNGT GDVLIGVPKP 900
WNDEPMANNPL TTLNLEHDD NHVGVQLVKA QTVIGSGGSL TLRDLQGDEV EADKTLHIAQ 960
NGTVVAEGDY GFRLTAPGD GLYVNYGLKA LNIHGGQKLT LAEHGGAYGA TADMSAKIGG 1020
35 EGDLAINTVR QVSLNGQND YQATYVQMG TLRTDADGAL GNTRELNIN AAIVDLNGST 1080
QTVEFTTQOM GSTVLFKEGS LTVNKGGISQ GELTGGGNLN VTGGTLAVEG LNARYNALTS 1140
VSPNAEVSLE NTQGLGRGNI ANDGLLTLKN VTGELRNSIS GKGIVSATAR TDVELDGDNS 1200
RFVQGQFNIDT GSALSVNEQK NLGDASVINN GLLTISTERS WAMTHSISGS GDLTKLGTGI 1260
LTLNNDSSAY QGTTDIVGGE IAFGSDSAIN TASQHINIHN SGVMSGNVTT AGDVNVMSGG 1320
40 TLRVAKTTIG ESAATWRMAA RFK 1343
<212> Type : PRT
<211> Length : 1343
SequenceName : SEQ ID 284
SequenceDescription :

Sequence

45 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
50 MGIKQHNGNT KADRLAELKI RSPSIQLIKF GAIGLNAILF SPLLIAADTG SQYGTNITIN 60
DGDRITGDTA DPSGNLYGVM TPAGNTPGNI NLGNDVTNV NDASGYAKGI IIQKKNSSLT 120
ANRLTVDVVG QTSAGINLI GDYTHADLGT GSTIKSNDG IIIGHSSTLT ATQFTIENS 180
GIGLTINDYG TSVDLGS GSK IKTDGSTGVY IGGLNGNNAN GAARFTATDL TIDVQGY SAM 240
GINVQKNSV DLGTNSSI KT SGD NAHGLWS FGQVSANALT VDTVGAANG VEVRGGTTTI 300
55 GADSHISSAQ GGGLVTS GSD ATINFSGTAA QRNSIFSGGS YGASAQTATA VINMQNTDIT 360
VDRNGSLALG LWALSGGRIT GDSLAIITGAA GARGIYAMTN SQIDLTS DLV IDMSTPDQMA 420
IATQHDDGYA ASRINASGRM LINGSVLSKG GLINLDMHPG SVWTGSSLS D NVNGGKL DVA 480
MNNSVWNVTS NSNLDTLALS HSTVDFASHG STAGTFTTLN VENLSGNSTF IMRADVVGE G 540
NGVKPWA 547
60 <212> Type : PRT
<211> Length : 547
SequenceName : SEQ ID 285
SequenceDescription :

Sequence

65 <213> OrganismName : Escherichia coli O157:H7

<400> PreSequenceString :
MGIDSRNDIP EGIATLGAFM GYSHSHIGFD RGGHGSVDSY SLGGYASWEH ESGFYLDGVV 60
KLNRFESNVA GKMSGGGAAN GSYHSNGLGG HIETGMRFTD GNWNLTPTYAS LTGFTADNPE 120
YHLSNGMESK SVDTRSIYRE LGATLSYNMR LGNGMEVEPW LKAAVRKEFV DDNRVKVNSD 180
5 GNFBVNDLSGR RGIYQAGIKA SFSSTLSGHL GVGYSNGAGM ESPWNAVAGV NWSF 234

<212> Type : PRT
<211> Length : 234
SequenceName : SEQ ID 286
10 SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
15 <400> PreSequenceString :
MKKKVLAIAL VTVFTGMGVA QAADVTAQAV ATWSATAKKD TTSKLVVTPL GSLAFQYAE 60
IKGFNSQKGL FDVAIEGDST ATAFKLTSRL ITNTLTQLDT SGSTLNVGVD YNGAAVEKTG 120
DTVMIDTANG VLGGNLSPLA NGYNASNRTT AQDGFTFSII SGTNGTTAV TDYSTLPEGI 180
WSGDVSVQFD ATWTS 195
20 <212> Type : PRT
<211> Length : 195
SequenceName : SEQ ID 287
SequenceDescription :

25 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MTAESYDDNY LDDEDADWTA TGQGQKSAGD TSFTLAWKPG EEGQKGLIGW FESGDVRAYK 60
30 IRFPNGTVDV FRGWVSSIGK AVTAKEVITR TVKVTNVGKP SVAEERSKIT PVSAIKVTPT 120
SGTVAKGKTT TLTVSFEPES ATDKTFRAVS ADPSKATISV KDMTITVNGV ATGKVQIPVV 180
SGNGQFAAVA EVTVTEAGAA G 201
<212> Type : PRT
<211> Length : 201
35 SequenceName : SEQ ID 288
SequenceDescription :

Sequence

40 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MTAESYDDNY LDDEDADWTA TGQGQKSAGD TSFTLAWKPG EEGQKGLIGW FESGDVRAYK 60
IRFPNGTVDV FRGWVSSIGK AVTAKEVITR TVKVTNVGKP SVAEERSKIT PVSAIKVTPT 120
SGTVAKGKTT TLTVSFEPES ATDKTFRAVS ADPSKATISV KDMTITVNGV ATGKVQIPVV 180
45 SGNGQFAAVA EVTVTEAGAA G 201
<212> Type : PRT
<211> Length : 201
SequenceName : SEQ ID 289
SequenceDescription :

50 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
55 MLYNIPCRIY ILSTLSLCIS GIVSTATATS SETKISNEET LVVTNRSAS NLWESPATIQ 60
VIDQQTQNS TNASIADNLQ DIPGVEITDN SLAGRKQIRI RGEASSRVLI LIDGQEVTYQ 120
RAGDNYGVGL LIDESALERV EVVKGPSVL YGSAIGGIV NFITKKGGDK LASGVVKAVY 180
NSATAGWEES IAVQGSIGGF DYRINGSYSD QGNRDPDGR LPNTNYRNNS QGVWLGYNNSG 240
NHRFGLSLDR YRLATQTYYE DPDGSYEAFS VKIPKLEREK VGVFYD TDVD GDYLLKKIHF 300
60 AYEQTIQRQF ANEVKTTQPV PSPMIQALTV HNKTDTHTDKQ YTQAVTLQSH FSLPANNELV 360
TGAQYKQDRV SQRSGGMTSS KSLTGFINKE TRRSYYESE QSTVSLFAQN DWQFADHWTW 420
TMGVRQYWLS SKLTRGDGVS YTAGIISDTS LARESASDHE MVTSTSLRYS GFDNLELRAA 480
FAQGVYFPTL SQLFMQTSAG GSVTYGNPDL KAEHSNNFEL GARYNGNQWL IDSAVYYSEA 540
KDYIASLICD GSIVCNGNTN SSRSSYYYD NIDRAKTWGL EISAEYNGWV FSPYISGNLI 600
65 RRQYETSTLK TTNTEGEPAIN GRIGLKHTLV MGQANIISDV FIRAASSAKD DSNGTETNVP 660
GWATLNFAVN TEFGNEDQYR INLALNNLTD KRYRTAHETI PAAGFNAAIG FVWNF 715

<212> Type : PRT
<211> Length : 715
SequenceName : SEQ ID 290
SequenceDescription :

5
Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
10 MTKMSRYALI TALAMFLAGC VGQREPAPVE EVKPAPEQPA EPQQPVPTVP SVPTIPQQPG 60
PIEHEDQTAP PAPHIRHYDW NGAMQPMVSK MLGADGVTAG SVLLVD SVNN RTNGSLNAAE 120
ATETLRNALA NNGKFTLVSA QQLSMAKQQL GLSPQDSLGT RSKAIGIARN VGAHYVLYSS 180
ASGNVNAPTL QMQLMLVQTG EIIWSGKGAV SQQ 213
<212> Type : PRT
15 <211> Length : 213
SequenceName : SEQ ID 291
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
20 MKSKVLALLI PALLGAGAAH AAEVYNK DGN KLDLYGKVDG LHYFSDNSAK DGDQSYARLG 60
FKGETQINDQ LTGYGQWEYN IQANNTESK NQSWTRLAFA GLKFSDYGSF DYGRNYGLDR 120
25 YAA 123
<212> Type : PRT
<211> Length : 123
SequenceName : SEQ ID 292
SequenceDescription :

30
Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
35 MATPNPLEPV KGAGTTLWVY NGKGDAYANP LSDDDWQRLA KVKDLTPGEM TAEPYDDNYL 60
DDEDADWTAT GQGQKSAGDT SFTLAWKPGE EGQKGLIGWF ESGDV RAYKI RFPNGTV DVF 120
RGWVSSIGKA VTAKEVITRT VKVTNVGKPS VAEERSEITP ATAIKVTPTS GTVAKGKTTT 180
LTVSFEPESA TDKTFRAVSA DPSKATISVK DMTITVNGVA TGVQIIPVVS GNGQFAAAVE 240
VTVTEAGAAG 250
40 <212> Type : PRT
<211> Length : 250
SequenceName : SEQ ID 293
SequenceDescription :

45
Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
50 MATPNPLEPV KGAGTTLWVY NGKGDAYANP LSDDDWQRLA KVKDLTPGEM TAEPYDDNYL 60
DDEDADWTAT GQGQKSAGDT SFTLAWKPGE EGQKGLIGWF ESGDV RAYKI RFPNGTV DVF 120
RGWVSSIGKA VTAKEVITRT VKVTNVGKPS VAEERSEITP ATAIKVTPTS GTVAKGKTTT 180
LTVSFEPESA TDKTFRAVSA DPSKATISVK DMTITVNGVA TGVQIIPVVS GNGQFAAAVE 240
VTVTEAGAAG 250
<212> Type : PRT
55 <211> Length : 250
SequenceName : SEQ ID 294
SequenceDescription :

60
Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MGWTDMLPEF GGSYTNADN FMTGRANGVA TYRNTDFGFL VNGLNFAVQY QGNNEGASNG 60
QEGTNNGRDV RHENGDWGL STTYDLGMGF SAGAA YTSSD RTNDQVNH TA AGGDKADAWT 120
65 AGLKYDANNI YLATMYSETR NMTPFGSDSY AVANKTQNFE VTAQYQFDFG LRPVASF LMS 180
KGRDLHAAGG ADNPA GVDDK DLVKYADVGA TYYFNKNMST YVDYKINLLD EDDSFYAANG 240
ISTDDIVALG L VYQF 255

<212> Type : PRT
<211> Length : 255
SequenceName : SEQ ID 295
SequenceDescription :

5 Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :

10 MGFIMKLTKT ALCTALFATF TFSANAQTYP DLPVGIKGGT GALIGDTVYV GLGSGGDKFY 60
TLDLKDPSAQ WKEIATFPFG ERNQPVAAAV DGKLYVFGGL QKNEKGELQL VNDAYRYNPS 120
DNTWMKLPTR SPRGLVGSSG ASHGDKVYIL GGSNLSIFNG FFQDTVAAGE DKAKKDEIAA 180
AYFDQRPEDY FFTTELLSYE PSTNKWRNEG RIPFSGRAGA AFTIQGNELV VVNGEIKPGL 240
RTAETHQKQF TAKGVQWKNL PDLPAKPKGS QDGLAGALSG YSNGHVLTG GANFPQSIKQ 300
15 FKEGKLHAKH GLSKAWHNEV YTLNNGKWRI VGELPMNIGY GFSVSYNNKV LLIGGETDGG 360
KALTSVKAIS YDGKKLTIE 379
<212> Type : PRT
<211> Length : 379
SequenceName : SEQ ID 296
SequenceDescription :

20 Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :

25 MGEQYMLTTI LSLIVTTTV AYVSWLKTG DDLKSSKGYF LAGRGLSGLV IGCSMVLTSI 60
STEQLIGVNA VSYKGNFSVI AWTVPTVIPL CFLALYIIGW L 101
<212> Type : PRT
<211> Length : 101
SequenceName : SEQ ID 297
SequenceDescription :

30 Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :

35 MKNQHKNPLT KALMKTYPYN HFLFFCFILG AFLLGLLSPA YALSIITTKE IDANLLNGAI 60
ESRVVLGKRV FKVEAHGFYF RNNATNSIDI EITSLLRDNQ SFPLTSSAKT SLKIPPNNAKI 120
KKSTILVLKG ENAEVAKIL GVSKEEYQKL ENIAQTKAAN DPMYANTPFS NGSDSSFYDN 180
40 NPNSPSNNAI NGKDGANGSN GYGANGNDGV NGISGSNGAN GSHSNNAIG SGIDTDGVLG 240
VDGVNGSSSS SGGSVGGYEN NFTNHGSTNN NTGGYDNFNN GSSSGGSLGN GGLFPPIPGN 300
GDTNNSNNST NNTSPTNGSS SNNATNPSSQ ENNYSSQYCK VPELSPNNTM KLDVIAKDGS 360
CISMNALRDD TKCAYRYDFE AGKAIKQTQY YYVDRENKTQ NIGGCVDLQG AQYAMQLYKD 420
DSKCALQTTT DKGYGMGKTQ TFQTEIVFRG MDNLIHVAVP CSDYARVQDR IVRYEKNDKT 480
45 QTLTPIVDQY YNDPNNPNKQ EILNRGIATQ LSSQYQEFAC QQWEYNDAKL EAKRPTMLKS 540
YNKLNGEWEV VTPCNFEAGI KSGAVVSPYV MGVPSSKVLS DITTSHYFRI ERKNYGEREQ 600
CQKLYGVNRC QPQYSILILV SPIGAPLTKP LPPKPLNLIY AQP KIMKNTP QPIILSPLKP 660
PSTGLKAF 668
<212> Type : PRT
<211> Length : 668
SequenceName : SEQ ID 298
SequenceDescription :

50 Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :

55 MPVIRVLVLM ATMMMLVKVT AKEKKVFKNV GISIMGIAFW EAIKDSIKKQ IKKSDWICGN 60
VKTADDYLKT HPNSWFNSAI GVTAITAMLM NVCFADDQSK KEVAQAQKEA ENARDRANKS 120
60 GIELEQEEQK TEQEKQKTEQ EKQKTEQEKQ KTEQEKQKTE QEKKQKTSNIE TNNQIKVEQE 180
QQKTEQEKQK TNNQKDLVN KAEQNCQENH NQFFIKKLG I KAGIAIEIEA ECKTPKPTKT 240
NQTPPIQPKHL PNSKQPHSQ RSKAQELIAY LQKELESPLP SQKAIKQVD FYRPSIAYL 300
ELDPRDFNAT BEWQKENLKI RSKAQAKMLE MRSCLKPDPQA HLSTSQSLLL VQKIFADVSK 360
EIKVVANTEK KVEKAGYGYS KRM 383
<212> Type : PRT
<211> Length : 383
SequenceName : SEQ ID 299

SequenceDescription :

Sequence

5 <213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MNYPNLPNSA LEISEQPEVK EITNELLKQL QNALRSNAHF SEQVELSLKC IVRILEVLLS 60
LDFFKNANEI DSSLRNSIEW LTNAGESLKL KMKEYERFFS EFNTSMHANE QEVNTNLNAN 120
AENIKSEIKK LENQLIETTT RLLTSYQIFL NQARDNANNQ ITKNKTQSLE AITQAKNNAN 180
10 NEISNNQTQA ITNITEAKTN ANNEISNNQT QAITNINEAK ESATTQINAN KQEAINNITQ 240
EKTQATSEIT EAKKTDHYQN IDFFEFE 267
<212> Type : PRT
<211> Length : 267
SequenceName : SEQ ID 300
15 SequenceDescription :

Sequence

20 <213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKFFSKDLFK KVTPLFLSVY FLSPTLTQAK SRFYVASQYQ VGKMIMKKYN DLKRTIEGAS 60
FSLGWEINPT NYWFYSRYYP FMDYGNVILN KRTGAQANMF TYGFGGDLIM EYNKNPLYVF 120
SLFYGMQVAE NTWTISKHSA NFIIDDWRSI QGFSLKTSNF RMLGLVGFKF QTVLFHHDAS 180
IEVGIKWPFA FEYDSPFVRL FSVFISHTFY L 211
25 <212> Type : PRT
<211> Length : 211
SequenceName : SEQ ID 301
SequenceDescription :

Sequence

30 <213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKKFTLSLFL CCTLLNAEED IFRNNTNETD LTNSFEHGKE NNNLIPAKSD SLESFKEQEN 60
35 KEKAKQIMDL KALQSVYFSK NRKLQDNNFN VLYVAGNTNK IRLRYAMTTT FIFDNDPIIY 120
VSLGDPDSFE LTYPTNDHYD LSNMLVIKPL LIGVDTNLT VV GASGTIYTL LFV 173
<212> Type : PRT
<211> Length : 173
40 SequenceName : SEQ ID 302
SequenceDescription :

Sequence

45 <213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MLDYVPWIGN GYRYGNNHRG SNSSTSGVTT QGQSQNASSN EPAPTFSNVG VGLKANVNGT 60
LSGSRTTFNQ QGTPWLTLTDQ ANLQLWTGAG WRNDKNGQSD ENYTNFASAK GSTNQGGSTT 120
GGSAGNPDSL KQDKADKSGD SVTVAEATSG DNLNTYTNLP PTSPPHPTDR TRCHSPTRTT 180
50 PSGCSCSCAA CWAASRCWSI RVGKMIVTSL IPPTKNGLTP N 221
<212> Type : PRT
<211> Length : 221
SequenceName : SEQ ID 303
SequenceDescription :

Sequence

55 <213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
60 MDDITAPQTS AGSSSGTSTN TSGSRSFLPT FSNVGVGLKA NVQGTLLGGRQ TTTTGNNIPK 60
WATLDQANLQ LWTGAGWRND KTTSGSTGNA NDTKFTSATG SGSGQGSSSG TSTSAGNPDG 120
LQADKVDQNG QVKTSVQEAT SGDNLNTYTN LPPANLTPTA DWPNALSFNT KNNQRAQLF 180
LRGLLGSIPV LVNKGQDDN SKFKAEDQKW SYTDLQSDQT KLNLPAYGEV NGLLNPAIVE 240
TYFGNTRASG SGNTTSSPG IGFKIPEQSG TINTSKAVLI TPGLAWTPQD VGNIVVSGTS 300
65 FSFQLGGWL VTFDFIKPRA GYLGLQLTGL DVSEATQREL IWAKRPWAAF RGSWVNRGR 360
VESVWDFKGV WADQAQLAAQ AATSSSTTTA TGATLPEHPN ALAYQISYTD KDSYKASTQG 420
SGQTSNQNS PYLHFIKPKK VESTTQLDQG LKNLLDPNQV RTKLRSFQGT DHSTQPPQS 480

LKTTTTPVFGR SSGNLSSVFS GGGAGGGSSG SGQSGVDLSP VERVSGH 527
<212> Type : PRT
<211> Length : 527
SequenceName : SEQ ID 304
SequenceDescription :

5 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
10 MLKLAVGIFI SPTLRFSTG FNLAGSVLDQ VLDYVPWIGN GHRYGNHNRG VDDITAPKTG 60
AGSSSGTSTN TSGSRSLPT FSNVGVGLKA NVQGTLLGGSQ TTTTGKDIPK WPTLDPANLQ 120
LWTQDGAWRND KASNKQSDEN HTTFKSATGS GQGGGSTTGG SAGNPDSLKQ DKISKSGQNL 180
TTQDGA PQSN STTESASND HLPNLTPTS DWPNALSTFN KNNAPRAQLF LRGLLGSIPV 240
15 LVNRSRGSDS NKFQATDQKW SYTDLKSDQT KLNLPAYGEV NGLNLPALVE TYFGTTRAGG 300
SGSNTTSSPG IGFKIPEQNN DS KAVLITPG LAWTPQDVGN LVVSGTSLSF QLGGLVLTFT 360
DFVKPRAGYL GLQLTGLDAS DATQRALIWA KRPWAAFRGS WVNRLGRVES VWDLKGWQD 420
QAQAAAQAAT TAAATGDALP EHPNALAYQI SSTDKDSYKA STQSSGQTNS QNTSPYLHLI 480
KPKKVENTTQ LDQGLKTCWT PTRFAPSCAK ALVQTIPPKP NPNPSKQPHR CLGRIVVTTA 540
20 VCLVVGVL EE QTAPIRWTSP PLNGWVGGLW GNYFVGVGGI VVRILKVCKT LLFISIFISI 600
FFLNCSLTFL IWTASLATG LTVVGHFTST TTTLKRQQFS YTRPDEVALR HTNAINPRLT 660
PWTYRNTSFS SLPLTGENPG AWALVRDNTA KGITAGSGSQ QTTYDPTRTE AALTATTTFV 720
LRRYDLAGRC TTSTFRS 737
<212> Type : PRT
<211> Length : 737
SequenceName : SEQ ID 305
SequenceDescription :

25 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
30 MLDYIPWIGN GHRYGNDHRG SNSSTSGVTT QGQQSQNASG TEPASTFSNV GVGLKANVQG 60
TLGGSQTTTT GKDIPKWPTL DQANLQLWTG AGWRNDKASS GQSDENHTKF TSATGSGQQG 120
35 SSSGTTSNAG NPDLSLKQDKV DKSGDSVTVA ETTSGDNLTN YTNLPPNLT TADWPNALSF 180
TNKNNAPRAQ LFLRALLGSI PVLVNKSGQD DSNKFQATDQ KWSYTELKSD QTKLNLPAYG 240
EVNGLNLPAL VEYGLSSTQ GSSTGAGGAG GNTGGDTNTQ TYARPGIGFK LPSTDSESSK 300
ATLITPGLAW TAQDVGNLVV SGTSLSFQLG GWLVTFTDFI KPRSGYLGLO LTGLDANDSD 360
QRELIWAPPA LNRSLWQLGQ PLGPRGECVG FQGGVGGSSS VRLASSYKYH HRNEGYLIGA 420
40 HQCFGLSGEL YRPGFVQGFH SKLRPKPKHL PLPALGAGEK SRFLW 465
<212> Type : PRT
<211> Length : 465
SequenceName : SEQ ID 306
SequenceDescription :

45 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
50 MLGSIPVLVN RSGSDSNKFQ ATDQKWSYTD LQSDQTKLNL SAYGEVNGLL NPALVETYFG 60
TTRTSSTANQ NSTVPGIGF KIPEQNND SK ATLITPGLAW TPQDVGNLVV SGTTVSFQLG 120
GWLVTFTDFV KPRAGYLGLO LSGLNASDSD QRELIWAPRP WAAFRGSWVN RLGRVESVWD 180
LKGWVADQAQ LAAQAATSS TTTATGATLP EHPNALAYQI SYTDKDSYKA STQSGQTNS 240
QNNSLYLHLI KPKKVESTTQ LDQGLKNLLD PNQVRTKLRLQ SFGTDHSTQP QPQSLKTTTP 300
55 VFGAMSGNLG SVLSGGGAGG AGSTNSVDLS PVERVSGSLT INRNFSY 347
<212> Type : PRT
<211> Length : 347
SequenceName : SEQ ID 307
SequenceDescription :

60 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
65 MGQGGQSGTS AGNPDSLKQD KISKSGDSL TQDGNATGQQ EATNYTNLPP NLTPADWPN 60
ALSFTKNNA HRAQLFLRGL LGSIPVLVNR SGSDSNKFQA TDQKWSYTDL QSDQTKLNL 120
AYGEVNGLLN PALVETYFGN TRAGGSGSNT TSSPGIGFKI PEQNND SKAT LITPGLAWTP 180

QDVGNLVVSQ TSLSFQLGGW LVSFTDFIKP RAGYLGLQLS GLDASDSDQR ELIWAKRPWA 240
AFRGSWVNRL GRVESVWDLK GVVADQAQLA AQAATSEASG SALAPHENAL AFQVSVVEAS 300
AYSSSTSSSG SGSSSNTSPY LHLIKPKKVE STTQLDQGLK NLLDPNQVRT KLRQSFGTDH 360
STQPQSLTT TPVFGTSSGN IGSVLSGGGA GGGSSGSGQS GVDLSPVERV SGH 413

5
<212> Type : PRT
<211> Length : 413
SequenceName : SEQ ID 308
SequenceDescription :

10
Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
15 MGLQLSGLDA SDSDQRELIW AKRPWAAFRG SWVNRLGRVE SVWDLKGWVA DQAHSAVSES 60
QAATSSSTTT ATGDTLPEHP NALAYQISS TDKDSYKASTQ GSGQTNSQNT SPYLHLIKPK 120
KVTASDKLDD DLKNLLDPNE VRVKLRQSFQ TDHSTQPPQ PLKTTTPVFG TNSGNLGSVL 180
SGGGTTQDSS TTNQLSPVQR VSGWLVGQLP STSDGNTSST NNLAPOINTG NEVVGVGDLS 240
KRASIESRL WIALKP 256

20
<212> Type : PRT
<211> Length : 256
SequenceName : SEQ ID 309
SequenceDescription :

25
Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
30 MRDNTAKGIT AGSGSQTTY DPARTEATLT TTFALRRYD LAGRALYDL FSKLNPQTPT 60
RDANCQITFN PFGGFGLSGS APQWNEVK KVPVEVAQDP TDPYRFAVLL VPRSVVYEQ 120
LQRGLALPNQ GSSSGSQQN TTIGAYGLK KNAEADTAKS NEKLQDESK SSGSSSTST 180
TTQRGSTNSD TKVKALKIEV KKKSDSEDNG QLQLEKNDLA NAPIKRGEES GQSVQLKADD 240
FGTAPSSSGS GGSNPNPSPT PWRPWLATEQ IHKDLPKWSA SILILVDAPY ARNRTAIDRV 300
DHLDPKVM TA NYPPSWRMPK WNHHLWDWK ARDVLFTQTG FDESNTSNTK QGFQKEADSD 360
35 KSAPIALPFE AYFANTGNLT WFGQALLVFG GNGHVTKSAH TAPLSIWLYI YLVKAVTFRL 420
LLANSLLSKS NIYKKTAN 438
<212> Type : PRT
<211> Length : 438
SequenceName : SEQ ID 310
SequenceDescription :

40
Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
45 MRDNIAGKIT AGSNTQTTY DPTREATLT TATTFALRRY DLAGRALYDL DFSKLNQPTP 60
TRDQTGQITF NPFGGFGLSG AAPQWNEVK DKVPVEVAQD PSNPYRFAVL LVPRSVVYEQ 120
QLQRGLALPN QGSSSGSQQN TTIGAYGLK VKNAEADTAK SNEKLQYES KSSNGSSSTS 180
TTQRGGSSNE NKVKALQVAV KKKSGSQGNS GDQTEQVEL ESNDLANAPI KRGSNNNQV 240
50 QLKADDFGTA PSSSGSGTQD GTPTPWPWL TTEQIHNDPA KFAASILILY DAPYARNRTA 300
IDRVLDHDPK VMTANYPPSW RTPKWNHGL WDWKARDVLL QTTGFFNPRR HPEWFDGGQT 360
VADNEKTGFD VDSENTKQG FQKEADSDKS APIALPFEAY FANIGNLTWF EQALLVFGIC 420
LS 422
<212> Type : PRT
55 <211> Length : 422
SequenceName : SEQ ID 311
SequenceDescription :

60
Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
65 MLWPFWRVWW KRVLTQTRA PAKPNPLTVP PTCTWWSLRK LPNPTKLDDD LKNLLDPNEV 60
RARMKLSFGT ENFTQPPQPP QALKTTTPVF GTSSGNLGSV LSGGGYHAGL KHHQSTVTRS 120
TGEWVDR 127
<212> Type : PRT
<211> Length : 127

SequenceName : SEQ ID 312
SequenceDescription :

5 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MRDNSAKGIT AGSESQTTY DPTRTEAALT ASTTFALRRY DLAGRALYDL DFSRLNPQTP 60
TRDQTGQITF NPFGGFGLSG AAPQQWNEVK NKVPVEVAQD PSNPYRFAVL LVPRSVVYYE 120
10 QLQRGLALPN QGSSSGSGQQ NTTIGAYGLK VKNAEADTAK SNEKLQGES KSSNGSSSTS 180
TTTQRGGSSG DTKVKALQVA VKKKSGSQGN SGEQTEQVE LESNDLANAP IKRGEESGQS 240
VQLKAADFQT TPSSSGSGGN SNPGSPTPWR PWLATEQIHK DLPKWSASIL ILYDAPYARN 300
RTAIDRVDDL DPKVMTANYP PSWRTPKWNH HGLWDWKARD VLLQTTGFFN SRRHPEWFDQ 360
GQAVADNTQT GFDTDDTDNK KTRLKSGSWL RQAGPDRPPV WSVLRQHWQP HTVRASAFGV 420
15 WDLFVLIN 428

<212> Type : PRT
<211> Length : 428
SequenceName : SEQ ID 313
SequenceDescription :

20 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
25 MFGLKVKNAE ADTAKSNEKL QGAETGSST TSGSGQSTQR GGSSGDTKVK ALQVAVKKKS 60
GSQGNSGDQG TEQVELESND LANAPIKRGs NPASPTQGSR LRHHPIQFGI WSIRHPHPLK 120
AVACDRANSQ GPPQMIRLDP HSVRCALCL 149

<212> Type : PRT
<211> Length : 149
SequenceName : SEQ ID 314
SequenceDescription :

30 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
35 MFGLKVKDAT VDSSKQSTES LKGEESSSSS TTSSTSTTQR GGSSGDTKVK ALQVAVKKKS 60
DSEDNGQIEL ETNNLANAPI KRGSNNNQV QLKADDFGTS PSSSESGQSG TPTPWTPLA 120
TEQIHKDLPK WSASILILYD APYARNRTAI DRVDHLDPKV MTANYPPSWR TPKWNHHGLW 180
40 DWKARDVLVQ TTGFFNPRRH PDWFDQGQAV AENTQTGFDT DDTDNKKQGF RKQGEQSPAP 240
IALPFEAYFA NIGNLTWFGQ ALLVFGICLS 270

<212> Type : PRT
<211> Length : 270
SequenceName : SEQ ID 315
SequenceDescription :

45 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
50 MGSQNGGSTT TTSAGNPDSL VTDKVDQKQ VQTSQNLSD TNYTNLSPNF TPTSDWPNAL 60
SFTNKNNQAR AQLFLHGLLG SIPVLVKNKG ENNEKFQATD QKWSYTELKS DQTKLNLPA 120
GEVNGLLNPA LVETIFYGTR TSSTANQNST TVPGIGFKIP EQNNDKAVL ITPGLAWTPQ 180
DVGNLVVSGT SFSFQLGGWL VSFTDFVKPR AGYLGLQLTG LDASDATQRA LIWAPPALSG 240
55 LSWQLGQPVG PRGECVGFEG GVGSSSVRL ARIYHHRNRG YLTGAPECFG LSGECGSEC 300
LQAKHELPRN PIH 313

<212> Type : PRT
<211> Length : 313
SequenceName : SEQ ID 316
SequenceDescription :

60 Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
65 MSFGLVGTVN NNGWKSPFRH ETKYRAGYDK FKYYKTHYRG AKKAGTNDNR WRWTAWFDLD 60
FAHQKIVLIE RGELHRQADL KKSDPATNET SKTVWGSIKE KLLQNVNNLH SEKGVFLWFR 120

QSGFTTTRN
<212> Type : PRT
<211> Length : 129
SequenceName : SEQ ID 317
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MAEPLAVDPT GLSAAAAKLA GLVFPQPPAP IAVSGTDSVV AAINETMPPI ESLVSDGLPG 60
VKAALTRTAS NMNAAADVYA KTDQSLGTSL SQYAFGSSGE GLAGVASVGG QPSQATQLLS 120
TPVSQVTTQL GETAAELAPR VVATVPQLVQ LAPHAVQMSQ NASPIAQTIS QTAQQAQSA 180
QGGSGPMPAQ LASAEKPATE QAEPVHEVTN DDQGDQGDVQ PAEVVAAARD QGAGGAGGQQ 240
PGGGVPAQAM DTGAGARPA SPLAAPVDPS TPAPSTTTTL 280
<212> Type : PRT
<211> Length : 280
SequenceName : SEQ ID 318
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MRYLIATAVL VAVVLVGWPA AGAPPSCAGL GGTVQAGQIC HVHASGPKYM LDMTFPVDYP 60
DQQALTDYIT QNRDGFVNVA QGSPLRDQPY QMDATSEQHS SGQPPQATRS VVLKFFQDLG 120
GAHPSTWYKA FNYNLATSQP ITFDTLFPVQ TTPLDISIYPI VQRELARQTG FGAAILPSTG 180
LDBAHYQNF A ITDDSLIFYF AQGELLPSFV GACQAQVPRS AIPPLAI 227
<212> Type : PRT
<211> Length : 227
SequenceName : SEQ ID 319
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MKMVKSIAAG LTAAAAIGAA AAGVTSIMAG GPVVYQMQPV VFGAPLEPLDP ASAPDVPTAA 60
QLTSLNLNSLA DPNVSFANKG SLVEGGIGGT EARIADHKLK KAAEHGDLPL SFSVTNIQPA 120
AAGSATADVS VSGPKLSSPV TQNVTFVNQG GWMLSRASAM ELLQAAGN 168
<212> Type : PRT
<211> Length : 168
SequenceName : SEQ ID 320
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTYSPGNPGY PQAQPAAGSYG GVTPSFAHAD EGASKLPMYL NIAVAVLGLA AYFASFGPMF 60
TLSTELGGGD GAVSGDTGLP VGVALLAALL AGVALVPKAK SHVTTVAVLG VLGVFLMVSA 120
TFNKPSAYST GWALWVVLAF IVFQAVAAVL ALLVETGAIT APAPRPKFDP YGQYGRYGQY 180
GOYGVQPGGY YGQQAQQA GLQSPGPQQS PQPPGYGSQY GGYSSSPSQS GSGYTAQPPA 240
QPPAQSGSQ SHQGPSTPPT GFPSFSPPPP VSAGTGSQAG SAPVNYSNPS GGEQSSSPGG 300
APV 303
<212> Type : PRT
<211> Length : 303
SequenceName : SEQ ID 321
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MKCPGVSDCV ATVRHDNVFA IAAGLRWSAA VPPLHKGDV TKLLVGAIAG GMLACAAILG 60
DGIASADTAL IVPGTAPSPY GPLRSLYHFN PAMQPQIGAN YYNPTATRHV VSYPGSFWPV 120
TGLNSPTVGS SVSAGTNNLD AAIRSTDGPI FVAGLSQGT LLDREQARLA NDPTAPPPGQ 180

LTFIKAGDPN NLLWRAFRPG THVPIIDYTV PAPAESQYDT INIVGQYDIF SDPPNRPGNL 240
LADLNAIAAG GYYGHSATAF SDPARVAPRD TTTTNSLGA TTTYFYRTD QLPLVRLVD 300
MAGLPPQAAG TVDAALRPII DRAYQGPAP AVNPRDLVQG IRGIPAIAPA IAIPIGSTTG 360
ASAATSTAAA TAAATNALRG ANVGPGANKA LSMVRGLLPK GKKE 404

5 <212> Type : PRT
<211> Length : 404
SequenceName : SEQ ID 322
SequenceDescription :

10 Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSTGCTTAAAG GPPFFDAIPN FIEDLDVIVA AAPPAPACST GVSAAQLGEI TSTTAAALAGQ 60
15 KAPHCPAESD QTPAGAAGDG DLPEVGGRVT SPPQPPVAAL TGYSANIGGL SVPHSWNLPP 120
AVRQVAAMFP GATPMYMTGS SDGSYAGLAA AGLAGTGLAG LAARGGSAPT PAAAAAPAGAG 180
GAGPAATRPA AQTTPAVPAA AAGSAIPGLP PGLPPGVVAN LAATLAAIPG ATIIIVPPSP 240
NANQ 244
<212> Type : PRT
20 <211> Length : 244
SequenceName : SEQ ID 323
SequenceDescription :

25 Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MDVALGVAVT DRVARLALVD SAAPGTVIDQ FVLDVAEHPV EVLTETVVGT DRSLAGENHR 60
LVATRLCWPD QAKADELQHA LQDSGVHDVA VISEAQAATA LVGAAGHAGSA VLLVGDETAT 120
30 LSVVGDEPDAP PTMVAAPVA GADATSTVDT LMARLGDQAL APGDVFLVGR SAEHTTVLAD 180
QLRAASTMRV QTPDDPTFAL ARGAMAAGA ATMAHPALVA DATTSLPRAE AGQSGSEGEQ 240
LAYSQASDYE LLPVDEYEEH DEYGAAADRS APLSRRSLLI GNAVVAFAVI GFASLAVAVA 300
VTIRPTAASK VEGHQNAQP GKFMPLLPQ QAPVPPPP DDPTAGFQGG TIPAVQNVVP 360
RPGTSPGVGG TPASPAPEAP AVPGVVPAPV PIPVPIIIPP FPGWQPGMPT IPTAPPTTPV 420
35 TTSATTPPTT PPTTPVTTTP TTPPTTPVTT PPTTPPTTPV TTPPTTVAPT TVAPTTVAPT 480
TVAPTTVAPA TATPTTVAPQ PTQQFTQQPT QQMTQQQTV APQTVAFAAQ PPSGGRNGSG 540
GGDLFGGF 548
<212> Type : PRT
<211> Length : 548
40 SequenceName : SEQ ID 324
SequenceDescription :

Sequence

45 <213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MKNARTLLIA AAIAGTLVTT SPAGIANADD AGLDPNAAAG PDAVGFDPNL PPAPDAAPVD 60
TPPAPEDAGF DPNLPPPLAP DFLSPPAEEA PPVPVAYSVN WDAIAQCESG GNWSINTGNG 120
50 YGGLRFTAG TWRANGSGS AANASREEQI RVAENVLRSQ GIRAWPVCGR RG 172
<212> Type : PRT
<211> Length : 172
SequenceName : SEQ ID 325
SequenceDescription :

55 Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
60 MTRLIPCTL VGLMLTLLPA PTSAAGSNTA TTLFPVDEV TLEHTFLDC HPNGSCDFVA 60
GANLRTPDGP TGFPPLWAR QTTEIRSTNR LAYLDAHATS QFERVMKAGG SDVITTVYFG 120
EGPPDKYQT GVIDSTNWST GQPMTDVNVV VCTHMVQVYP GVNLTSPSTC AQANFS 176
<212> Type : PRT
65 <211> Length : 176
SequenceName : SEQ ID 326
SequenceDescription :

Sequence

5 <213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTPGLLTAG AGRPRDRCAR IVCTVFIETA VVATMFVALL GLSTISSKAD DIDWDAIAQC 60
ESGGNWAANT GNGLYGGLQI SQATWDSNGG VGSPAAASPQ QQIEVADNIM KTQGPRAWPK 120
CSSCSQGDAP LGSLLHILTF LAAETGGCSG SRDD 154
10 <212> Type : PRT
<211> Length : 154
SequenceName : SEQ ID 327
SequenceDescription :

Sequence

15 <213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MMQQAIVSGIT GALGGAVGGV MGELTQLPQQ AMQAGQGAMQ PLMSALQQTY GAEGLDVADG 60
ARLVDSIEGE PGLGGEPEGAG DVGAGGGGGG TTPTGYLGPP PVPTSSPPTT PAGAPAKSVT 120
20 PDPVSGTFRA SGPAGMTGMP MVPPGALGAG AEGANKDKPV EKRVTGCAEW STGQGPIINST 180
AECSGEICRR QAGGHQVDAT DPCCAERRQG 210
<212> Type : PRT
<211> Length : 210
SequenceName : SEQ ID 328
25 SequenceDescription :

Sequence

30 <213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MIRELVTTAA ITGAAIGGAP VAGADPQRYD GDVPGMNYDA SLGAPCSSWE RFIFGRGPSG 60
QAEACHFPPP NQFPPAETGY WVISYPLYGV QQVGAPCPKP QAAAQSPDGL PMLCLGARGW 120
QPGWFTGAGF FPPEP 135
<212> Type : PRT
35 <211> Length : 135
SequenceName : SEQ ID 329
SequenceDescription :

Sequence

40 <213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MKTTGTTIKL GIVWLVLVSF TVMLIIVVFGQ VRFHHTTGYS AVFTHVSGLR AGQFVRAAGV 60
EVGKVAKVTI IDGDKQVLVD FTVDRLSLSD QATTASIRYL NLIGDRYLEL GRGHSQRLA 120
45 PGATIPLEHT HPALDLALL GGFRLPFQTL DPKVNSIAS SIITVFQGGG ATINDILDQT 180
ASLTATLADR DHAIGEVVNN LNTVLATTVK HQTEFDRTVD KLEVLITGLK NRADPLAAAA 240
AHISSAAGTL ADLLGRIVHC CTAASGTSRA SSSRS 275
<212> Type : PRT
<211> Length : 275
50 SequenceName : SEQ ID 330
SequenceDescription :

Sequence

55 <213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTPRSLVRIV GVVVATTLAL VSAPAGGRAA HADPCSDIAV VFARGTHQAS GLGDVGEAFV 60
DSLTSQVGGG SIGVYAVNYP ASDDYRASAS NGSDDASAH QRTVASCPNT RIVLGGYSQG 120
ATVIDLSTSA MPPAVADHVA AVALFGEPSG GFSSMLWGGG SLPTIGPLYS SKTINLCAPD 180
60 DPICTGGGNI MAHVSYVQSG MTSQAATFAA NRLDHAG 217
<212> Type : PRT
<211> Length : 217
SequenceName : SEQ ID 331
SequenceDescription :

65

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MISTTRIDFL WILSVAFASM IALATLLTLI NQVVGTPYIP GGDSPAGTDC SELASWVSNA 60
ATARPVFGDR FNTGNBEEAAL AARGFQQGTA PNALVIGWNG HHTAVTLPDG TPVSSGEGGG 120
5 VRVGGGGAYQ PKFTHHMYLP MDVDAGEDQP PAPDEPVTAV DDVEPEMPAP CPTQRPPVTP 180
RHNLCNKLRT MPGALSAALA AAAPVWPAPI SGRGFSTSL LAKRNHPVIV GK 232

<212> Type : PRT
<211> Length : 232
10 SequenceName : SEQ ID 332
SequenceDescription :

Sequence

15 <213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTTMITLRRR FAVAVAGVAT AAATTVTTLAP APANAADVYG AIAYSGNGSW GRSWDYPTRA 60
AAEATAVKSC GYSDCKVLTS FTACGAVAN DRAYQGGVGP TLAAAMKDAL TKLGGGYIDT 120
WACN 124
20 <212> Type : PRT
<211> Length : 124
SequenceName : SEQ ID 333
SequenceDescription :

25 Sequence

30 <213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MAGLNIYVRR WRTALHATVS ALIVAILGLA ITPVASAATA RATLSVTSTW QTGFIAFTI 60
TNSSTAPLTD WKLEFDLPAG ESVLHTWNST VARSGTHYVL SPANWNRIIA PGGSATGGLR 120
GGLTGSYSPP SSCLLNGQYP CT 142
<212> Type : PRT
<211> Length : 142
SequenceName : SEQ ID 334
35 SequenceDescription :

Sequence

40 <213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MLTRAIKTQL VLLTVLAVIA VVVLGWYFLR IPSLVGIGRY TLYAELPRSG GLYRTANVTY 60
RGITIGKVTG VEPTERGARA TMSIDNGYQI PTDASANVHS VSAVGEQFVD LVSTRTSGPY 120
LRHGQTITTT TVPSQIGPAL DAANRGLAVL PKDRVASVLH EASEAVGGIG SSLNRLIEAT 180
QAIAHDVRGS LEDIDDIER SAPIIDSQVN SCNEIARWAA NLNTLAAQTA QTDPAVRSL 240
45 ANAAPTADQV NATFSDVRES LPQTLANLEV VIDMLKRYHN GVEQALVFLP QSGAIAQSVT 300
TEFFPGQAGLG VGGLALNQPP PCLTGFLPAS EWRSPADTST APLPKGTYCR IPMDASNVVR 360
GARNNPCVDV PGKRAATPRE CRSNEAYVPG GTNPWYGDPN QMLSCPAPAA RCDQPVKPGQ 420
VIPAPSVNNG INPLPADQLP GTPPPVNDPL QRPGSGTVQC NGQQPNPCVY TPSTFPTTIY 480
DVQSGKVVP DGVVYSVEAS THAGADGWKV MLAPTG 516
50 <212> Type : PRT
<211> Length : 516
SequenceName : SEQ ID 335
SequenceDescription :

55 Sequence

60 <213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
MLNNTQFLNL MKSYMKEPEFY MSSIKNTTNL DLSSITNTIQ KAMNIFFTTN KISTESMQSL 60
FKKNSEIQN NINTILNSTK EVINSKDFKQ ATEYHQKCVK SIYETSMDNA KELANIAEYA 120
SNKIFEAAANK HITKNIHNAS NNIHNTAEQV QKNFNNKSA 159
<212> Type : PRT
<211> Length : 159
SequenceName : SEQ ID 336
65 SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
5 MNIKLVTYFL ILVSSLKVNA DLNHIQDSFK YQAEQLTIE LPWNDCTAIH KFLEEKLFPS 60
EQQIKKENKI HEKYKQFYLO HNNKLSDFSM QFLEKKSEIN SVETLISGFL KFCEDNFQTS 120
KSKSHSLNFF QKQQDQWLHN IRNENYKTTY KKKYEDNTFR NIN 163
<212> Type : PRT
<211> Length : 163
SequenceName : SEQ ID 337
10 SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
15 <400> PreSequenceString :
MKKLLLIATA SATILSSSVS FAECIDNEWY LRADAGVAMF NKEQDKATGV KLKSNKAIP 60
DLGIGYYISE NVRADLTIGT TIGGKLKKYG AATNTHFTGT NVSVSHKPTV TRLLINGYVD 120
LTSFDMFDVF VGGGVGPALV KEKISGVSGL ASNTKNKTNT SYKLIFGTSA QIADGVKVEL 180
AYSWINDGKT KTHNVMYKGA SVQTGGMRYQ SHNLTGVGRF GI 222
20 <212> Type : PRT
<211> Length : 222
SequenceName : SEQ ID 338
SequenceDescription :

25 Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
30 MKKNMRKQML KIISIIIIISL LLSSCSESTR DENGLLTDSQ STIIRDYIIS QNSKNLKVNL 60
KEKFGSNLKG VKLIGIKLTN EDLSGIDFTS CEILRTDFMG SNLEKAILTN SVIQESNFAD 120
SVIKNISGYN ADFQGSIFNN ITLQNTNFVQ SNFSDTAFNK STIINVNFEN SKFSNVLWCH 180
SNIDSSNFQK THLKNNSFKN TNVMNSIFYG ADLGKSVINN TNFTNNYFES SDLSNTKFTS 240
VLIKDSNFTQ SIFNSVNFNN IQSNNSFFSY TSFEDSTLHN IHLTKCDLQN STINSSVFNN 300
FKIDNAILTN MSLNDNTFNN LSIKNSNTNF VRINKSKGFN ITLLNTNYSN AIFSNNDLKE 360
35 PKVINTDLNN SEIINSNFTN GQFNNVNFSS SLIQNVNFTD VKITLGNLQ VALINSNLIN 420
TNIINSVLBN SQINNINYQA YYSFINTNVS NNIVINDNSN QIPPNIVIN SEKDLQNISN 480
LANMNLTFN LSNLVPNGVD FSKSIFKKAN LTNTVIKNSI LKDNFSAAI LTKTDFSKSI 540
LTGSIFKFAQ IDQTCFSNSD LTNTDFTEAT IKNTAFDNAN THGKIGLE 588
40 <212> Type : PRT
<211> Length : 588
SequenceName : SEQ ID 339
SequenceDescription :

Sequence

45 <213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :
MIQKFTNVKL NDMRKILSFL MMCSLHLGLQ SQTWHGDPDS VAALPSIGIQ ESSCTRITFE 60
VVFPGFYSVE KREGNQVFQR ISMPGCGSFG NLGEAELPVL KKMIAVPEFS TANVAVKIKE 120
50 TETFDNYNIY PNPTYVVEEL PEGGTYLVEA FAINNDYYSQ NVSLPSTHYV YSQDGYFRSQ 180
RFIEVTLYPF RYNPVRQEIL FAKKIEVTIT FDNPPPLQK NTGIFNKVAS SAFINYEADG 240
KSAIENDMVF SRGTTYISG NVASNLPQNC DYLVIYDDMF NVNQPHDEI KRLCEHRAFY 300
NGFDVAAVSI KDVLNSFPSN ATSYINETKL KNFIRSVYNQ SNAKRTLDGK LGYVLLIGKP 360
LSKYLADTDN TKVPTSFHNN VSLIPSHPTF GSICADSYFF SCVSPLDTVG DLFGRFSVT 420
55 NAHELHNLIE KTINKAISYN PIAHKNIYA EGKGCDAPI RLFLKEIASG YTVNSILKSN 480
QVSAIDSIFD CLNNGSHHFP FNTGGMPTVW GIGQGLDVNT LTARLNTTSS QGLCTSLSCS 540
SAVADSTIRS LGEVLTTYAP NKGFS AFLGG SRATQYAVYL EGPCPPSEFY EYLPYSLYHN 600
LSTVVGEMLL SSIINTNSVD TYSKFNFNLL GDPALNIMAH GMEVSNCTIL PNNTIISPI 660
TIKNGGCLKI PEKGVLFHTN NGSIQVMSGG TLEIGNQAKI SGETGANPTF ITVYGDGLAI 720
60 NKQVEIDNID RLNLFTHSV MPKPHFDSVK FNSAPLYTTN CIVEISNCEF TNRSDIISK 780
CDLSVENSMP SSSGITVFKP MATSSITGLS TKAKITDNTF FATGNFAYHI TNTPGLTATS 840
NAAIKLDNIP EYVISGNKIV NCDEALVLNN SGNRTNRLHN ITRNVKNCR IGSTLYNSYG 900
IYNRNKISNN HIGVRLNNS CFYFDNAPVI NEEDKQTFIS NRTWQLYSSN GTFPLNFHYN 960
SLQGGDTDTW IYNDTYTNR IYDVSNNHWGN NDLEFDPNQVF NTPDLFIWIP FWDGLPNGRS 1020
65 GNSSAEAVEF QTALDCIGNS DYLSAKVALK MMVETYPESD FAIAALKELF RIEKMSGNDY 1080
EGLKDYFRSN PTIISQNLF PTADFLSARC DIVCENYQSA IDWYENRLNS EISYQDSVFA 1140
VIDLGDYWN MQLDSLRTG IDLNILSCEQ RKSLESHQNV KNYLLSTLPE STGTLLPPL 1200

CNKSSLDKSK IISISPNAK AVVTIIYYTD NPSCSVIKIY GINGASADIT GLPKHLSEGY 1260
YSIQFNTSNF DPGFYLVTLN VDQKIIDTEK LRIK 1294
<212> Type : PRT
<211> Length : 1294
5 SequenceName : SEQ ID 340
 SequenceDescription :

Sequence

10 <213> OrganismName : Shigella flexneri 2a str. 2457T
 <400> PreSequenceString :
MQGKNTIVTT GDYSIGLLSQ TSGNLNTDTI IRVNSDGSVT PSFSDGDDTF IVTAGNHA VG 60
VLACASPGSA CACVSSLDEE STADTGSNEN NAIAKLDMAK GEITTHGTES YAAYANGTVV 120
KAGDTLDYTN ASVTLLTDVDI TTHGDNAHAI AARQGTVSFN QGEFYTTGPD AAI AKIYNGG 180
15 TVTLKNTSAV AHQSGGIVLE SSINGQEATV DILSGSSLRS ANELIYHKDE TSNVTITDSE 240
VSSAADVFIN NIKGHLTVDA TNSKITGSAN ISTDDNTHTY LSLSDNSTWD IKADSTVSNL 300
TVDNSTVYIS RADGRDVEPT RLITITENYVG NNGVLHLRTE LDDDNSATDK VVINGNTSGT 360
TRVKVTNAGG SGAYTLNGIE IISVEGESNG EFIKDSRIFA GAYEYSLTRG NTEATNKNWY 420
LTNFQATSGG ETNSGGSSAP TVAPTPVLRP EAGSYVANLA AANTLFVMRL NDRAGETRYI 480
20 DPVTEQERSS RLWLRQIGGH NAWRDSNGQL RTTSHRYVSQ LGGDL LTGGF TSDSDSWRLGV 540
MAGYARDYNL THSSVSDYRS KGSVRGYSAG LYATWFADDI SKKGAYIDSW AQYSWFKNSV 600
KGDELAYESY SAKGATVSLE AGYGFALNKS FGLEAAKYTW IFQPQAQAIW MGVDHNAHTE 660
ANGSRIENDA NNNIQTRLGF RTFIRTQEK N SGPHGDDFEP FVEMNWIHNS KDFAVSMNGV 720
KVEQDGVSNL GEIKLGVNGN LNPAASVWGN VGVQLGDNGY NDTAVMVGLK YKF 773
25 <212> Type : PRT
 <211> Length : 773
 SequenceName : SEQ ID 341
 SequenceDescription :
30 Sequence

 <213> OrganismName : Shigella flexneri 2a str. 2457T
 <400> PreSequenceString :
35 MTKLKLLALG VLIATSAGVA HAEGKFSLGA GVGVEHPYK DYDTDVYPVP VINYEGDNFW 60
FRGLGGGYL WNDATDKLSI TAYWSPLYFK AKDSGDHQM R HLDDRKSTMM AGLSYAHFTQ 120
YGYLRITTLG DTLDNSNGIV WDMAWLYRYT NGGLTVP TGI GVQWNS ENQN EYYGVSRKE 180
SARSGLRGYN PNDSWSPYLE LSASYNFLGD WSVYGTARYT RLSDEVTDSP MVDKSWTGLI 240
STGITYKF 248
40 <212> Type : PRT
 <211> Length : 248
 SequenceName : SEQ ID 342
 SequenceDescription :
45 Sequence

 <213> OrganismName : Shigella flexneri 2a str. 2457T
 <400> PreSequenceString :
50 MKKIALAGLA GMLLVASVN AMSISGQAGK EYTNIGVGFG TESTGLALSG NWTNDDDDGD 60
VAGVGLGLNL PLGPLMATVG GKGVYTNPNY GDEGYAAAVG GGLQWKIGNS FRLFGEYYS 120
PDSLSSGIQS YEEANAGARY TIMRPVSIEA GRYRLNLSGK DGNRDNAVAD GLYVGVNASF 180
 <212> Type : PRT
 <211> Length : 180
55 SequenceName : SEQ ID 343
 SequenceDescription :

Sequence

60 <213> OrganismName : Shigella flexneri 2a str. 2457T
 <400> PreSequenceString :
MTTLTARVFT TAEIIYRKTV IALVCHLNCS RQETVTM NKT IMALAIMMAS FAANASVLPE 60
TPVPFKSGTG AIDNDTVYIG LGSAGTAWYK LDTQAKDKKW TALAAPGGP REQATSAFID 120
GNLYVFGGIG KNS EGLTQVF NDVHKYNPKT NSWVKLMSHA PMGMAGHVT F VHNGKAYVTG 180
65 GVNQNI FNGY FEDLNEAGKD STAI D KINAH YFDKKAEDYF FNKFLLSFDP STQQWSYAGE 240
SPWYGTAGAA VVNKGDKTWL INGEAKPGLR TDAVFELDFT GNNLKWNKLD PVSSPDGVAG 300
GFAGISNDSL IFAGGAGFKG SRENYQNGKN YAHEGLK KSY STDIHLWHNG KW D KSGELS Q 360

GRAYGVSLPW NNSLLIIGGE TAGGKAVTDS VLISVKDNKV TVQN 404
<212> Type : PRT
<211> Length : 404
SequenceName : SEQ ID 344
5 SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
10 <400> PreSequenceString :
MATGGAALAG KAVMGAAAGA AGGASALQAA FQKASASMET GGDMSMSGSV VSSGGNNGGGE 60
AGTAGSSPFA QAAGFGDSGS SSSGGGFAKA AKLATGTASE LAKGVGSQVK QGFQERVSET 120
TGGKLAASIR ESMEPKASQ SGQFEGNSLG ADSGPDSENEV RS 162
<212> Type : PRT
15 <211> Length : 162
SequenceName : SEQ ID 345
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRVLIPGVI LCGADVAQAV DDKNMYMYFF EEMTVYAPVP VPVNGNTHYT SESIERLPTG 60
NGNISDLLRT NPAVRMDSTQ STSLNQGGDIR PEKISIHGAS PYQNAYLIDG ISATNNLNPA 120
25 NESDASSATN ISGMSQGYL DVSLLDNVTL YDSFVPVEFG RFNNGVIDAK IKRPNADDSK 180
VKLGVRTTRL DWLTSIDEN KNSAFNQGSS GSTYFSPDFK KNFYTLNFSNQ ELADNFGVTA 240
GLSRRQSDIT RADYVSNDSI VAGRAQYKNV IDTALSKFTW FASDRFTHDL TLKYTGSSRD 300
YNTSTFPQSD REMGNKSYGL AWDMDTQLAW AKLRRTTVGWD HISDYTRHDH DIWYTELSCT 360
YGDITGRCTR GGLGHISQAV DNYTFKTRLD WQKFAVG DVS HQPYFGAEYI YSDAWTERHN 420
30 QSESYVINAA GKKTNHTIYH KGKGLGIDN YTLYMADHIS WRNVSLMPGV RYDYNLYLSN 480
HNISPRFMTI WDIFADQTSI ITAGYNRYYG GNILDMGLRD IRNSWTESVS GNKTLTRYQN 540
LKTPYNDELA MGLQKIDKN VIARASEAHD QISKSSRTDS ATKTTITEYN NDGKTKTHSF 600
NLSFELAEPL HIRQVDINPQ IVFSYIKSKG NLSLNNGYEE SNTGDNQVVY NGNLVSYDSV 660
PVADFNNPLK ISLNMDFTHQ PSGLVWANTL AWQEARARI ILGKTNAQYI SEYSDYKQYV 720
35 DEKLDSSLTW DTRLNTPQF LKQQNLITISA DILNVLDSTK AVDTTNTGVA TYASGRFTFWL 780
DVSMKF 786
<212> Type : PRT
<211> Length : 786
SequenceName : SEQ ID 346
40 SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
45 <400> PreSequenceString :
MKKTLALIML AGTAFASQAG TLVSQGTAS ANLTLTKPIV VNNTIQPVKG VYSGTLTAWT 60
PLATGIVGAS DGQSHDYAVT FPDDIYAESS TSADAVISGD NNPDKHLKVS LTTLEQDPPS 120
AASEEIGGKR YMMLKNTGTG GAYRVVSHMK EQVVEPDSYT IRTQAYIYAE 170
<212> Type : PRT
50 <211> Length : 170
SequenceName : SEQ ID 347
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
55 <400> PreSequenceString :
MGIYHWSRKT KMKRTKSIRH ASFRKNWSAR HLTTPVALAVA TVFMLAGCEK SDETVSLYQN 60
ADDCSAANPG KSAECTTAYN NALKEAERTA PKYATREDCV AEFGEQGCQQ APAQAGMAPE 120
60 NQAQAQSSG SFWMPLMAGY MMGRMLGGGA GFAQQPLFSS KNPASPAYGK YTDATGKNYK 180
AAQPGRTMTV PKTAMAPKPA TTTTVTRGGF GESVAKQSTM QRSATGTSSR SMGG 234
<212> Type : PRT
<211> Length : 234
65 SequenceName : SEQ ID 348
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
15 MTKMSRYALI TALAMFLAGC VGQREPAPVE EVKPAPEQPA EPQQPVPTVP SVPTIPQQPG 60
PIEHEDRTAP PAPHIRHYDW NGAMQPMVSK MLGADGVTAG SVLLVDSVNN RTNGSLNAAE 120
ATETLRNALA NNGKFTLVSA QQLSMAKQQL GLSPQDSLGT RSKAIGIARN VGAHYVLYSC 180
ASGNVNAPTL QMQLMLVQTG EIIWSGKGA V SQQ 213
<212> Type : PRT
10 <211> Length : 213
SequenceName : SEQ ID 349
SequenceDescription :

Sequence

15 <213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MTKLMQFVQR CYYMTNKKMY FILILVFTLL QVCFFALWKA RDGSTTSLEC TSTLTRNAKT 60
DHSLYYSANL SVILKKDGS SFTIVGLTDE DTPRKFSHSY FFTYKIDSNG RISGNAKAKV 120
20 SGLENQIKDE NFRNLNPLDAS LTGKGNARLS KFNNVYIFSI PGLIINTCAP I 171
<212> Type : PRT
<211> Length : 171
SequenceName : SEQ ID 350
25 SequenceDescription :

Sequence

30 <213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MGRISSGGMM FKAITTVAAAL VIATSAMAQD DLTISSLAKG ETTKAAFNQM VQGHKLPAPV 60
MKGGTYTPAQ TVTLGDETYQ VMSACKPHDC GSQRIAMWS EKSNNQMTGLF SAIDEKTSQE 120
KLTWLNVNDA LSIDGKTVLF AALTGSLENH PDGFNFK 157
<212> Type : PRT
35 <211> Length : 157
SequenceName : SEQ ID 351
SequenceDescription :

Sequence

40 <213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKQFLEKAV FTVAATAATV VLGKMKADAD TYTLQEGDSF FSVAQRYHMD AYELASMNGK 60
DITSLILPGQ TLTVNGSAAP DNQAAAPTDT TQATTETNDA NANTYPVGQC TWGVKAVATW 120
45 AGDWWGNGGD WASSASAQGY TVGNTPAVGS IMCWTDDGGY HVAYVTAVGE DGKVQVLESN 180
YKDQQWVDNY RGWFDPNNSG TPGSVSYIYP N 211
<212> Type : PRT
<211> Length : 211
SequenceName : SEQ ID 352
50 SequenceDescription :

Sequence

55 <213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MSIKNILENK TTTIKVSFAG IATAASLILP MAVQAETTYT VKSGDTLSEI ASTHGTTVDK 60
LAKLNKINNI HLIHAGQILE LDAATEDTDA TPVQESQINE AETSASAKTS QTSEVTTTAP 120
VQESQTSEVI TSAPAETSQT SEVPTEANQT NEVSSAVSVE TSQTSEATTS APVETSQTSE 180
ATTAEPTETK TSQTNEVAAS AEENQTTSTNT SGLSTSDAAA KEFIAQKESG GNYNAKNGQY 240
60 YGRYQLSDSY LNGDLSEENQ ERVADAYVSS RYGSWTAAQA FWNANGWY 288
<212> Type : PRT
<211> Length : 288
SequenceName : SEQ ID 353
SequenceDescription :
65

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKCQAFEDFK ATSLNKLSTY TGGATDGEII ANRMLQ GKAT KGEITMYTWN IIQNGWVNSL 60
VSWGIGGYNS SIGYSAQGNR GFSNYPYDVS MDSDNSSSSS NTGGYVNYN QSFNSGW 117

5
<212> Type : PRT
<211> Length : 117
SequenceName : SEQ ID 354
SequenceDescription :

10
Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
15 MRYSQICRKS LALLATGMIL TTSTLPSISI LAEDSTGAPA RPDQAPAGG GANTTTYDYS 60
GINSGLVAN GSKVTSSSKT KSTTSAQNTA LVQNGGSLTL HKANLIKSGD DNNGDNDNFY 120
GINSILLAVN ERSKAYVNSN KLKASSSGSN GIFATDKATI YANKTSIATT ADNSRGLDAT 180
YNGNIIANKM AISTKGAHSA AIATDRGGGN ISTTNSSLNT SGSGSPLLYS TGNIQVNHVT 240
GTSSNSQIAG MEGLNTILIH NSNLISTMTN KTASDPIANG VIIYQSQSGD AEATTGQSAH 300
20 FELSKSKLTS SITSGSMFYI TNSANIILN QSTLNPDANK AKLLTVAGNS ANNWGTPGSN 360
GATVNFTHGK QTLKGDVDVD SISTLNMYLL DKTNYTGKTA VSTNSTNIS STSPITMNIS 420
KNSKWLTGH STVTNLNAEK GAKIVDKDGK TVSVISSSQG KLVKGKSKYS LTVGTYSQK 480
VTTSSSNKPS SSIYINRSDFD NYFKTTTAFV NNTKNTSN 518
<212> Type : PRT
25 <211> Length : 518
SequenceName : SEQ ID 355
SequenceDescription :

30
Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MNKIGDTLRD ARIEKLSTF DVVDKGTIAP HYILLAMELDQ LKLLPEGKTN EYLEKYAHAV 60
GLDPVSIHIG YRNQEMSDEL ILPSSAELAA SSDSNIEKKN EGKSIEEPQE LAIDSLDVTQ 120
35 NITEETPQIE DFKVESEES KKIEKIPSR SKYDYDEEPK KKFPWALILL ILLALTIISY 180
VGYYVYNQLQ TDSNKTSTL STKSKDTKN DANSTTQST SITTFADGG NNITLSNTNG 240
KVEVTFTLTG DEESWVSATN TTDGESGTTT TATDKTYTVT LAEGSTTSM LTVGSPSGVEI 300
TINGQKVDTT NLVNAGLTNI NLTVQ 325
<212> Type : PRT
40 <211> Length : 325
SequenceName : SEQ ID 356
SequenceDescription :

45
Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKSRRQRKRG LVRKNEIIL TLFVASAVSL LAFTNSFGVL AKSLHLEKIN KSITISLPFG 60
KKKMEQTARY YSGEQVQISS SAKKDSLKG LSHYQNWIGT VKKIKSQKDS RQKHHSYEV 120
50 TFDNGKALKY VQEKDLVTK RSKYSKGQIV KLKSSATADL DGSSLTDYRA SAGKIDHISY 180
NHSNTTGGYK YDITFDEGK VTNIEKDL KVEVQLKSE NTAAQNNEIL KQAFAYAKQH 240
SGTILSLPNG EFKIGSQTPD KDYITLSTDT EIRGDNTLL VEGSAYWFAF ATGTSASDGV 300
KNFTMRNINI KASDLEKGNQ FMIMADHGDN WKICNNSFTM VHKKGSHIFD LGSLSNSAFE 360
GNQFTGYAPE LTNVSKIDDN ADLHDFYSEV IQLDAAESSG VWDGGLIKAI DPNYENYNKE 420
55 KQLCENNITIA NNSFVPYIDS HGKIIAYSGT IGQHSSDVGL VKIYDNVFSN SLVSRFNQNG 480
KSEAWIFKAI HLKSNYNNV YANSIS 506
<212> Type : PRT
<211> Length : 506
SequenceName : SEQ ID 357
60 SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
65 <400> PreSequenceString :
MRKLKVALFA SSILGMLAVS SYTAADTEDN QVTISHYNEQ AGTFDVNAVQ AANGKTIQSI 60
DVAIWSEENG QDDLKWHAS NDGSNQLTVH FNAENHGSKV GSYIAHAYIT YTDGNRVGVN 120

LGKRKLSLSA PQLSLKQGG LQFSKLKPSA ADQLFSAVWS DENGQDDLHW YTADADGNTL 180
AGYANHKGYG TYHVHTYLKQ NGKMIPISAQ DIDIPKPKVK IQIDKINDTS YDVVVNNVPP 240
YISSVAIPVW SEQNGQDDLK WYQATKVADG IFKTTVYLKT HRFELGNYQA HIYGDSQLSK 300
KLDGLGETHF NVPSTIINYED PQVTIDHYNI NKGTDFVTVA ETDNSKAIQS ISAAVWSDAN 360
5 QANLYWYEAK QLANGKAAIT VDVQKHGNQT GSYNVHVYVH YNDGTTSGHV LANQQLNQIV 420
HYQPSAVRIT AYMNEKNTYP VGQCTWGVKE LAPWIPNWLG NGGQWASTVA VKGFKIGTVP 480
KVGAIACWSD GGYGHVAVYT HVESNNRIQV KEANYKNQQY ISNFRGWFD P TTSYLGRLTY 540
IYPD 544
<212> Type : PRT
10 <211> Length : 544
SequenceName : SEQ ID 358
SequenceDescription :

Sequence

15 <213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MANNYSRRQQ PTKKTGTSR KRPTEHIKTG FSALQKSAI IAGILGIITA LITINNYRNS 60
SHNDKKDSTS KTTIIEKEV DDSNSNNNA NSQAENDSNN NNNSAESNQ N QTATTANDSN 120
20 SNSANQNQAN SQSQANNQON QNNANAGQ 148
<212> Type : PRT
<211> Length : 148
SequenceName : SEQ ID 359
SequenceDescription :

25 Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
30 MKIFSFGTIR NNTALKPNYD DTAFTSGFGT IRNNTALKQS TNCASWFNRF GTIRNNTALK 60
LTLILINGVSF CFGTIRNNTA LKPRGPIFVS TFRNRAIHLS QISASK 106
<212> Type : PRT
<211> Length : 106
SequenceName : SEQ ID 360
35 SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
40 <400> PreSequenceString :
MKRRKRNLYFL IGLFLTVFLL IGCSMQKKTK SESSSTSQKT TLQTKQSSEK STDAKQTTEA 60
HSESSQSSSH SNNEETLAPI DTGAVLKADY SSMAGTWKNE EGQTLTFDQR GLTTPGMTVS 120
LLNIDQDGNL LLNVETGTTK NLTLYIVPAN KTLNQQYFSN GQSDSDKTK DRIVSSESLN 180
SGKFTNRVYY HVSTH 195
45 <212> Type : PRT
<211> Length : 195
SequenceName : SEQ ID 361
SequenceDescription :

50 Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MTPKKIKIAL TALISLMLAL FLFLFNHHSV RENSQQEKLK ISKASSKKSQ TSTSSVMTSS 60
55 RKATEQTSQA QTQSQSQA EQ SNP NVILPIP QELVGTYKGS SPQASEITFT ISSNGQLRAQ 120
ANFDPASDIN DVTATVSGVR KVGADTYIWE FVSGSSAALL PGVTGIGGLG KMQPGFILKG 180
GQLTPIMFTG SVDGEIDYSH PNPYPVSLNK Q 211
<212> Type : PRT
<211> Length : 211
60 SequenceName : SEQ ID 362
SequenceDescription :

Sequence

65 <213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKIINVIVL SLSVFFLIAC SNSSTGEKTS QSSEETKVRL IVKTDNKT D EKVAFKKGAT 60

VMDVLKDNKY VKESGGFITT IDGVTQDKKA GRYWMFDVND KLASKAADKI KVKNGDKIEF 120
YLKVKYGKN 129
<212> Type : PRT
<211> Length : 129
5 SequenceName : SEQ ID 363
 SequenceDescription :

Sequence

19 <213> OrganismName : Streptococcus mutans UA159
 <400> PreSequenceString :
MSNKPWEEKV TDATTDNEEM TRNSKDASII STPILTILLS LFFLLIIGIL FFVLYTSNGG 60
SNEKAATSGF YSSSKTVKKA KNEANSQTDE QTTEAETSSS ETTSSSSSDS GETITVQGGE 120
GAAAIARAG ISVDKLYELN PEHMTGHWY ANPGDNIKIK 160
15 <212> Type : PRT
 <211> Length : 160
 SequenceName : SEQ ID 364
 SequenceDescription :

20 Sequence

 <213> OrganismName : Streptococcus mutans UA159
 <400> PreSequenceString :
25 MPDNRMYISI DSNMQFPLVE ITLETGEFAY IQRGSMVYHT PSVTLNNTKVN GRGSGLGKLV 60
GAIGRSVTSG ESFFITQAVS NASDGKLALA PSMGPQVIAL ELGEKQYRLN DGAFLALDGS 120
AQYQMAQSV GRALFGGQGG LFMVTTEGQG TLLANSFSGI KKIQLNQEI TIDNAHVVAW 180
SRDLNVDIHL ENGFMQSIGT GEGVVNTFRG TGEIYVQSLN LQQFAGVLQG FITNTNR 237

 <212> Type : PRT
30 <211> Length : 237
 SequenceName : SEQ ID 365
 SequenceDescription :

Sequence

35 <213> OrganismName : Streptococcus mutans UA159
 <400> PreSequenceString :
MKNKYFWYGL LGLLALYLIT IAFIPGFHIF FSNMLMLALF FMLIALSNRS IFFFFLALGF 60
LSIYLDIFH FDYSTGPLFT GIIIGVILN SFLKPHYSYS YKGNHYFNMK QHANYIDNET 120
40 DVFLKTLFSE NTSYVTSQEL NKIIIDTKFG EQSVDSLQAQ FMTDSPEIHI DVSFGETNLR 180
IPNNWKLINK THSPFASISF SGFPSTNGDF INVTLTGTVA MGSLLNIQY 228
 <212> Type : PRT
 <211> Length : 228
 SequenceName : SEQ ID 366
45 SequenceDescription :

Sequence

50 <213> OrganismName : Streptococcus pneumoniae R6
 <400> PreSequenceString :
MKSITKKIKA TLAGVAALFA VFAPSFVSAQ ESSTYTVKEG DTLSEIAETH NTTVEKLAEN 60
NHIDNIHLIY VDQELVIDGP VAPVATPAPA TYAAPAAQDE TVSAPVAETP VVSETVVSTV 120
SGSEAEAKEW IAQKESGGSY TATNGRYIGR YGSWTAANKF WLNNGWY 167
 <212> Type : PRT
55 <211> Length : 167
 SequenceName : SEQ ID 367
 SequenceDescription :

Sequence

60 <213> OrganismName : Streptococcus pneumoniae R6
 <400> PreSequenceString :
MKHSHKKSFD WYSMQQRYSI RKYYFGAASV LLGTALVLGA AASVQTVQAE ENKQETNSI 60
SVGRGEAATK PAEVSASNKE KTYAAPTVAN PVETTPVKTE EVTKPAEKVE EAKDKKEEVT 120
65 HQDAVDKSL LTALSRAKKL ESKLYTEASA ANLQTSIQAG QSLLGKADAT EAELSAEASS 180
IQSFIIGLEL RSNKNETVS ETPVAKKADA VESKEGAKPA ATTERSADVS AILPTSTADK 240
VETTSAPASI NEILKLGLSL SDARQNPAIR KEDVNRGYSG FRAASNPNP IVSGSGNTVA 300

	FADISQGGRS	YSFRGYGNSR	GGNSIHYDVT	TVRSGNSVNF	TISYSAPGDS	REFVNNNFIL	360
	DKGDGFGNPS	NATITSSNPR	VREQSKSISQ	GANYVSHSGY	SMTSAISTNT	EQTIRFSLPI	420
	INLNGDLSVR	LKPVTFNVDQ	GGGGAATSND	PYSNSNYYYR	ANPLYLDANP	YGGTNNKTVS	480
	EDIDFTVYL	PTSKLPEGQT	RLVREGEKGQ	RQITYKVHRF	GNETLLGLPI	SNSVTKEAKP	540
5	RIMQIGVAKD	LIDTVKPRVD	QNKVGDITNNL	TFYLDNDGNG	VYTEGVDELV	QKIALKDGAK	600
	GEKGDQGERG	LITGAKGEKG	RGERGLTGAQ	GAKEGKDRG	ERGLTGAQGA	KGEKGRGER	660
	GLTGAQGAKE	EKGDRGERGL	TGAQGAKEG	GAQGERGLTG	AQGAKEKGD	QGERGLTGAQ	720
	GAKEGKDDQG	ERGLTGAQGA	KGEKGAQGER	GLTGTQGAKE	EKGDRGERGL	TGAQGAKEG	780
	GDRGERGLTG	AQGAKEKGA	QGERGLTGAQ	GAKEGKDDQG	ERGLTGAQGE	KGDRGERGLT	840
10	GAKEGKDDQG	ERGITGAKGE	KGAQGERGLT	GAQGAKEGK	DQGERGLTGA	QGEKGAQGA	900
	GRDGVTPTVT	VKDNKNDGTH	TITINDGRGN	VTSTVVRDGF	DGASPLVATQ	RNDADKTTTV	960
	IFYDYKNGNN	ELDASDKKLL	EVVIADGAKG	EKGDKEQGL	QGRDGEQGP	GEDGKTPTVK	1020
	VTDGQDGTHT	ITINDGKGR	TTTTVVRDGF	GASPLVSTHR	NEADKTTTVI	FYYDLNDNNQ	1080
	FDEGDTKLKE	VVIADGKQGP	KGDKGDMGFD	GFTPEVTVTD	NNNGTHTITI	TQPDNRPSLT	1140
15	TIVKNGEDGK	TPKVKAERDD	AKKQTTLTFF	IDKDGDSY	AGKDELVQTT	VVKDQDQGA	1200
	GASGRDKEV	LNGKVDPTTE	GKDGDTFVNT	QTGDFVFKKG	NTWEPAGNIK	GPKGDKGADG	1260
	AKGEKGAQGA	RGALTGAQGV	GEKGDQGERG	LTGSLTVEKG	QGERGLTGAQ	GAKEGKQGG	1320
	LQGRDGAQGP	KGADGQGP	GPQGPKEGQ	NPQTPGKDGK	SLIAVKNVGL	VTTITPVEGRP	1380
	QTTTFVEDGQK	GADGKTPTVT	ITEGQNGTHT	LTVHNPSPD	VTTTIRDGAT	GQAGRDGKDV	1440
20	LNGKVNPPQN	QKNGDKYIN	IETGDVYVKN	NGNWDKEGNI	KGPKGDKGAD	GAKEGKDDQG	1500
	ERGLTGAQGA	KGADGAVGRD	GRDGKDVNLG	KANPEAHQK	DGDYVNTET	GDVFKNNGN	1560
	WDKEGNIKGP	KGDKGADGAK	GEKGRGERG	LTGAQGAKE	DGAAGRDRD	GRDGKDVNLG	1620
	KVNPEANQGG	DGDYVNTET	GDVFKNNGN	WDKEGNIKGS	KGDKGERGED	GKTPEVTVTP	1680
	GKDGHSDDIT	FTVPGKDPVT	VNVKDGNG	NGKTPKVDLL	RVQKNGNPS	HTIVTFYTDE	1740
25	NNDGKTYFPT	DELGSEMIK	DGAKGADGRD	GKSLTVEKDG	KETKVYQEDP	ANPGQPLNPE	1800
	KPLAVIRGTV	DGKSPTVTAV	RKDEAGHKGV	EITVDNHDGS	QPTTVFVQDG	AKGKTGATGQ	1860
	DGQTPITTTQ	RGQDQGSTVV	TITTSKDPV	TFTVKDGKNG	KDGRAPKIKV	EDITSPSRIR	1920
	RDTDAATPT	RNGIRVTYD	DVNDNGVYDE	GVDKVLNSKD	IYNGIDGRD	SAPTITTKDN	1980
	GDGTHITTVQ	NPDGSESTTV	VKDGDGKTA	NITTFENPDG	SHTITVTNPD	GSTKETVVK	2040
30	GKDGKTPKVE	VTDNNDGTH	VKVTDDGNG	TNAIKDGK	GKAATATTTE	NPDGSHVTI	2100
	TNPDGKTNEF	VVKNGRDGVD	GRTPASVRD	NGDGSHITVI	TNPEGVTTE	TVRDGKSPKV	2160
	TITDEQNGTH	KISVLNGDGT	TTETIIKDGK	SPVATVRDNG	DGTYTIRVEN	GNGTVSETTV	2220
	RDGKSPYAKV	VNDGDGTHI	TVVNSDGITT	TTTVRDGREG	KLEVIDNNDG	SHTIKVTGAD	2280
	GKGTITITFD	GKSPKANIVD	NGDGTHITLI	VDSGREGYKS	IKDGKDGK	SVSPTVTVK	2340
35	NNDGTHVVTI	TNPDGSKTEM	VIKDGDKGS	PKVSVEDNGD	GSHTITIINS	DGTVTKTVIK	2400
	DGKDGDRDGR	GRDGKDGKDG	KCGCQDKPVT	PSNDKVPVPT	PNVPTPEVPV	KPVPAQPTPN	2460
	VPTPEVPVQ	TPAVSTPEVP	VKPVPAVPEQ	PVPTPAQPA	TPVNPANPVAP	TTGKENRGDK	2520
	LPETGSQSDY	ISVLLGSGIL	LSLYVGRRKE	D			2551
	<212> Type : PRT						
40	<211> Length : 2551						
	SequenceName : SEQ ID 368						
	SequenceDescription :						
	Sequence						
45	-----						
	<213> OrganismName : Streptococcus pneumoniae R6						
	<400> PreSequenceString :						
	MKKRMLLAST	VALSFAPVLA	TQAEVLWTA	RSVEQIQNDL	TKTDNKTSYT	VQYGDITLSTI	60
	AEALGVDVTV	LANLNKITNM	DLIFPETVLT	TTVNEAEEVT	EVBIQTPQAD	SSEEVTTATA	120
50	DLTTNQVTV	DQTVQVADLS	QPIAEAPKEV	ASSSEVTCTV	IASEEVAPST	GTSVPPEEQA	180
	ETSSAVAEAA	PQETTPAEKQ	ETQTSPPQAS	AVEATTSSE	AKEVASSNGA	TAAVSTYQPE	240
	ETKIIISTTYE	APAAPDYAGL	AVAKSENAGL	QPQTAAFKEE	IANLFGITSF	SGYRPGDSGD	300
	HGKGLAIDFM	VPERSELGDK	IAEYAIQNMA	SRGISYIIWK	QRFYAPFDSK	YGPANTWNPM	360
	PDRGSVTENH	YDHVHVSMMG					380
55	<212> Type : PRT						
	<211> Length : 380						
	SequenceName : SEQ ID 369						
	SequenceDescription :						
	Sequence						
60	-----						
	<213> OrganismName : Streptococcus pneumoniae R6						
	<400> PreSequenceString :						
	MTILGKDTVQ	QSAKGESVTQ	EATPEYKLEN	TPGGDKGGNT	GSSDANANEG	GGSQAGGSAH	60
65	TGSQNSAQSQ	ASKQLATEKE	SAKNAIEKAA	KNKQDEIKGA	PLSDKEKAEL	LARVEAEKQA	120
	ALKEIENAKT	MDVKEAETI	GVQAIAMTV	PKRPVAPNAA	PKTTSAPQAT	AGTMQDVTYQ	180
	SPAGKQLPNT	GSASSAALAS	LGLVVATSGF	ALLGRKTRRR	K		221

<212> Type : PRT
<211> Length : 221
SequenceName : SEQ ID 370
SequenceDescription :

5 Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :

10 MMTTGCSMGA YHALNFFLQH PDVFTKVIALL SGVYDARFFV GDYYNDDAIY QNSPVDYIWN 60
QNDGWFIDRY RQAEIVLCTG LGAWEQDGLP SFYKLKEAFD KKQIPAWFAE WGHDDVAHDWE 120
WWRKQMPYFL GNLVL 135

<212> Type : PRT
<211> Length : 135

15 SequenceName : SEQ ID 371
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :

20 MNKGLFEKRC KYSIRKFSLG VASVMIGATF FGTSPVLADS VQSGSTANLP ADLATALATA 60
KENDGHDFFA PKVGEDQGSF EVDGPKTEE ELLALEKEKP AEEKPKEDKP AAAPETPKT 120
VTPWQTVVEK KEQQTGTVIR BEKGVRYNQL SSTAQNDNAG KPALFEKKGL TVDANGNATV 180
25 DLTFKDDSEK GKSFRGVFLK FKDTKNNVVFV GYDKDGFWE YKSPTTSTWY RGSRVAAPE 240
GSTNRLSITL KSDGQLNASN NDVNLFDITV LPAAVNDHLK NEKKILLKAG SYDDERTVVS 300
VKTDNQEGVK TEDTPAEKET GPEVDDSKVT YDTIQSKVLK AVIDQAFPRV KEYSLNHGT 360
PGQVQQFNQV FINNHRTPE VTYKKINETT AEYLMKLRRD AHLINAEMTV RLQVVDNQLH 420
FDVTKIVNHN QVTPGQKIDD ERKLLSSISF LGNALVSVSS DQTGAKFDGA TMSNNTHVSG 480
30 DDHIDVTNPM KDLAKGYMYG FVSTDKLAAG VWSNSQNSYG GGSNDWTRLT AYKETVGNAN 540
YVGHSSEWQ WEKAYKGIVF PEYTKELPSA KVVITEDANA DKKVDWQDGA IAYRSIMNPN 600
QGWWKVKDIT AYRIAMNFGS QAQNPFLMTL DGIKKINLHT DGLGQGVLLK GYGSEHDSG 660
HLNYADIGKR IGGVEDFKTL IEKAKKYGAH LGIHVNASET YPESKYFNEK ILRKNPDGSY 720
SYGWNWLDQG INIDAAYDLA HGRLARWEDL KKKLGDGLDF IYVDVWGNQ SGDNGAWATH 780
35 VLAKEINKQG WRFALWGHG GEYDSTFHHW AADLTGYGYT NKGINSATR FIRNHQKDAW 840
VGDIRSYGGA ANYPLGGYS MKDFEGWQGR SDYNGYVTNL FAHDMVTKYF QHFTVSKWEN 900
GTPYTMNDNG STYKWTPEMR VELVDADNNK VVTRKSNDV NSPQYRERTV TLNLRVIQDG 960
SAYLTPWNWD ANGKLLSTDK EKMYFNTQA GATTWTLPSP WAKSKVLYK LTDQKTEEQ 1020
ELTVKDGKIT LDLLANQPYV LYRSKQTNPE MSWSEGMHIY DQGFNSGTLK HWTISGDASK 1080
40 AEIVKSQGAN DMLRIQGNKE KVSILTQKLTG LKPNTKYAVY VGVDNRSNAK ASITVNTGEK 1140
EVTYTNKSL ALNYVKAYAH NTRRNATVD DTSYFQNMVA FFTTGSVSN VTLTSLREAG 1200
DEATYFDEIR TFENNSSMYG DKHDTGKGTG KQDFENVAQG IFPFVVGVE GVEDNRTHLS 1260
EKHDPYTQRG WNGKKVDDVI EGNWSLKTNG LVSRRLVYQ TIPQNFREFE GKTIRVTFEY 1320
EAGSDNTYAF VVGKGEFQSG RRGTAQSNLE MHELNPNTWD SKKAKKATFL VTGAETGDTW 1380
45 VGIYSTGNAS NTRGDSGGNA NFRGYNDMM DNLQIEEITL TGKMLTENAL KNYLPTVAMT 1440
NYTKESMDAL KEAVFNLSQA DDDISVEEAR AEIAKIEALK NALVQKKTAL VADDFASLTA 1500
PAQAQEGLAN AFDGNLSSLW HTSWGQDVG KPATMVLKEA TEITGLRYVP RGSNGNLR 1560
DVKLVVTTDES GKEHTFTATD WPDNNKPKDI DFGKTIKAKK IVLTGKTYG DGGDKYQSA 1620
ELIFTRPQVA ETPLDLSGYE AALAKAQKLT DKDNQEEVAS VQASMKYATD NHLLTERMVE 1680
50 YFADYLNQLK DSATKPDAPT VEKPEFKLSS VASDQKTPD YKQETARPET PEQILPATGE 1740
SQFDALFLA SVSLALSALF VVKTKKD 1767

<212> Type : PRT
<211> Length : 1767
SequenceName : SEQ ID 372
SequenceDescription :

55 Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :

60 MKLYNKSELR YSRIFDKRP PAFAFILIIS TAILSGALV GAAYIPKNIY VKANGNSVIT 60
GTEFLSAISS GKVVTLHKSE GDMVNAGDVI ISLSSQEGE QASSLNKQLV KLRKEAIFQ 120
KFEQSLNEKY NRMSNSGEEQ EYVGKVEYYL SQLNSENYNN GTQYSKIQDE YTKLNKITAE 180
RNQLDADLQT LQNELIQLQQ QGDSPLSDT TSADKAKLE TKILEITTKI EALKTNITSK 240
65 NSEIDSQSN IKDMNRTYND PTSQAYNIYA QLVSELTAR SNNKKSITEL EANLGVATGQ 300
DKAHSILAPN EGTLYLVLPL KQMSIQQQQ TIAEVSGKEK GYYVEAFVLA SDISRVSKGA 360
KVDVAITGVN SQKYGTLLKGQ VRQIDSGTIS QETKEGNISL YKVMIELETL TLKHGSETTV 420

LQKMPVEVR IVYDKETYLD WILEMLSFQK 450
<212> Type : PRT
<211> Length : 450
SequenceName : SEQ ID 373
SequenceDescription :

5 Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
10 MNKGLHRIIF SKKHSTMVAV AETANSQGGK KQAGSSSVSVS LKTSGLDLCGK LKTTLKTLVC 60
SLVSLSMVLPA AHAIITTDKS APKNQOVVIL KTNTGAPLVN IQTPNGRGLS HNRYTQFDVD 120
NKGAVLNDDR NNNPFLVKGS AQLILNEVRG TASKLNGIVT VGGQKADVII ANPNGITVNG 180
GGFKNVGRGI LTIGAPQIGK DGALTGFDFVR QGTLTVGAAG WNDKGGADYT GVLARAVALQ 240
15 GKLQKKNLAV STGPQKVDYA SGEISAGTAA GTKPTIALDT AALGGMVADS ITLIANEKGV 300
GVKNAGTLEA AKQLIVTSSG RIENSRIAT TADGTEASPT YLSIETTEKG AAGTFISNGG 360
RIESKGLLVI ETGEDISLRN GAVVQNNGSR PATTVLNAGH NLVIESKTNV NNAKGSANLS 420
AGGRTTINDA TIQAGSSVYS STKGDTELGE NTRIIAENVV VLSNGSIGSA AVIEAKDTAH 480
IESGKPLSLE TSTVASNIRL NNGNIKGGKQ LALLADDNIT AKTTNLNTPG NLYVHTGKDL 540
20 NLNVKDLASA ASIHLSKSDNA AHITGTSKTL TASKDMGVEA GLLNVNTNTNL RTNSGNLHIQ 600
AAKGNLQDRN AELKPLAGRL TTALQGNIVS DGLHAVSADG HVSLLANGNA DFTGHNTLTA 660
KADVNAGSVG KGRLLKADNTN ITSSSGDITL VAGNGIQLGD GKQRNSINGK HISIKNNGGN 720
ADLKNLNVHA KSGALNIHSD RALSIENTKL ESTHNTLHNA QHERVTLNQV DAYAHRHLSI 780
TGSQIWQNDK LPSANKLVAN GVLALNARYS QIADNTTLRA GAINLTAGTA LVKRGNNINWS 840
25 TVSTKTLEDN AELKPLAGRL NIEAGSGTTL IEPANRISAH TDLSIKTGGK LLLSAKGGNA 900
GAPSAQVSSL EAKGNIRLVT GETDLRSGSKI TAGKNLVVAT TKGKLNIEAV NNSFSNYFPT 960
QKAAELNQKS KELEQQIAQL KKSSEPKSLI PTLQEERDRL AFYIQAINKE VKGKKPKGKE 1020
YLQAKLSAQN IDLISAQGIE ISGSDITASK KLNLAHAAGVL PKAADSEAAA ILIDGITDQY 1080
EIGKPTYKSH YDKAALNKPS RLTRGTGVSI HAAAALDDAR IIIIGASEIKA PSGSIDIKAH 1140
30 SDIVLEAGQN DAYTFLKTKG KSGKIIRKTK FTSTRDHLIM PAPVELTANG ITLQAGGNIE 1200
ANTTFNAPA GKVTLVAGEE LQLLAEGBIH KHELDVQKSR RFIGIKVGKS NYSKNEINET 1260
KLPVRVVAQT AATRSWWDTV LEGTEFKTTL AGADIQAGVG EKARVDAKII LKGIVNRIQS 1320
EEKLFTNLT VQKQAGRGST IETLKLPSFE SPTPPKLSAP GGYIVDIPKG NLKTEIEKLS 1380
KQPEYAYLKQ LQVAKNINWN QVQLAYDRWD YKQEGLTEAG AAIIALAVTV VTSGAGTGAV 1440
35 LGLNGAAAAA TDAAPASLAS QASVSFINNK GDVGKTLKEL GRSSTVKNLV VAAATAGVAD 1500
KIGASALNNV SDKQWINNLT VNLNAGSAA LINTAINGGS LKDNLDGAAL GAIVSTVHGE 1560
VASKIKFNLS EDYITHKIAH AIAGCAAAAA NKGKCQDGA I GAAVGEIVGE ALTNGKNPAT 1620
LTAKEREQIL AYSKLVAGTV SGVVGDDVNT AANAAKVAIE NNLLSQEEYA LREKLIKKAK 1680
GKGLLSLDWG SLTEQEARQF IYLIEKDRYS NQLLDTRYQKN PSSLNQEKI ILAYFINQTS 1740
40 GGNTAWAASI LKTPQSMGNL TIPSKDINNT LSKAYQTLRS YDSFDYKSAV AAQPALYLLN 1800
GPLGFSVKAA TVAAGGYNIG QGAKAISNGE YLHGTVPVVN GTLMVAGSVS AQAATSAKPA 1860
PVTRYLSNDS APALRQALTA ESQRIRMKLP BEYRQIGNLA IAKIDVKGLP QRMEAFSSFO 1920
KGEHGFISLP ETKIFKPISV DKYHNIAAPP RGTLRNIDGE YKLETTIAQQ LGNNRNVSGR 1980
IDLFTELKAC QSCSNVILEF RNRYPNIQNL IFTGK 2015
45 <212> Type : PRT
<211> Length : 2015
SequenceName : SEQ ID 374
SequenceDescription :

50 Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
55 MDLIQTPNKQ FVDGDRRTPG TPVPAWNLNQ LQGEYSILN AVGIEPNKAD HAQVLSAIKT 60
LAADASQVAS IDALRKYSST GYVNVNAYHA NTTVGGGVFV ADKADKSTAD NGCTVIIVSTD 120
GTRWRKVFSG MLNLHDFGYV ASKNNALSTL NAAESAALDV VVDCLGLSID TGNIYPQKNK 180
YTNGKFVING KTVDVQYQPI RSGIGRFISG TGAAANLKSN EWTGAGLVI GEGAMEQMEK 240
CVSSIAIGDR AQGFSKVS RD NIAIGADSLI NVQAATEWYD QSRMEGTRNI GIGGNAGRGI 300
TSGYSNVSIG RNAGQGLGEG SSNIALGAGA MAGTAPVGFS GDIEVFWPSS TSRTIAIGEA 360
60 VLQTYQGRAA QTAIGANAAR NTKKAEEKVTA IGSAAMENLE RNRAPNGGDV VWTGTEAGTY 420
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TATGAELKY VYSVNSTATK NEELTIIGAN AMNKALTAGY STIIGVDAAL LGDNYQKTTA 540
IGASSLRTGS HISTTAIGYW VIPLASSEKC VAIGDSAGYR NVQGDFTLTK ITNSIAIGYG 600
ARINDNEIQ IGTGQTLTA PTAVNIRSDG RDKADV KPLT NGLDFVMKLG PMTGYD RRD 660
65 SYVDELFDL PADERADKVR EWWANPIKG SHKEDRLRHV FIAQDIAALE DEYGRPLPMVN 720
KTNDTYTVEY ETFIPVLTKA IQEMAARIET LETEMKESKK 760
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<211> Length : 760
SequenceName : SEQ ID 375
SequenceDescription :

5 Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
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STITVETGPV QRPTVTTYTH PKFIDPIVTT LTGKTLSSLQ KPKDIVITGG IEILGFTLNN 120
SRQEKNYRSI TITVPEKTSI NEVKGSNVPH TTLSNLTVDQ MQFDGNLTLL HTKVKKATIT 180
GMLEATKSQL TNLELKADYS FSNLTDSSVE NGTISLNGQ LTTKDTTLKA INIQLHPGG 240
IEAERTTLEN VTFTVSKSKE EEEENDYYDN DAIFTAHALT LKGTNTISGG DIDVDITLTK 300
AKAIAYRART ENGKVSLSQ LTPAKIGKES TSDVISYVAE NKAATGNLTV NLNKGDTIK 360

15 <212> Type : PRT
<211> Length : 360
SequenceName : SEQ ID 376
SequenceDescription :

20 Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
25 MFKKENLKQR YFNFGALVALA LTILAIIFAF SSKNADTKSY AKKSESKMVT IDKAPKNNHA 60
ITKEESKEKA KSIASEPIPT VENSVAPTVT EEAPVVQDEV TQTVQQVSSV AYNPNNVVLS 120
NGNTAGIVGS QAAQMAAAT GVPQSTWEHI IARESNGNPN AANASGASGL FQTMPGWGST 180
ATVEDQVNAA LKAYSAGLS AWGY 204

30 <212> Type : PRT
<211> Length : 204
SequenceName : SEQ ID 377
SequenceDescription :

35 Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
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DKSLTIGNDM VDKMSKSKDL DYHFVSSKSA QKGLKKGDYY MVITLPEDLS QRATTLNPE 120
40 PQKLTRYQT SKGHGMVAAK MGETAMAKLK ESVSQNTKT YTSVAVSSMT DLQSGLKES 180
TGSQALDSGA KTAQMGSQL SDNLAGLSA SWQFQQTNR LTSGLTAYTA GVSQVKDGLG 240
QLSTDMPVYL NGVSRLSQA SQLNQGLSQL TQSTTSLDDK AKRIQSLEVG LPVLNQGIQQ 300
LNENLSTMVQ PKLNTDELGN NLAAIAQAAQ QLLVKEAAAH KEQLAVLQAT SAYQSLTAEQ 360
QGELTAALTQ TDKGEAVAPA QTILRSVQTL STSLQSLSQE DQSKQLEQLK EAVAQIANQS 420
45 NQALPGASSA LTELSTGLAK VNGSLNQVQL PGSNQLTTGL AQLNRYNTAI GSGVIKLESG 480
ANALSSKSGE LLDGSHQLSE GATKLADGSS QLSQGGHQLT SGLTELSTGL SILNGSLAKA 540
SQQLSLVSVT DKNKAVAKP LVLNEKDKDG VKTNGIGMAP YMIAVSLMVV ALSTNVIFAN 600
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MALVTALVGW DDRYGSFASL VMLLLQVGSS GGSYPIELSG AFFQKLHPFL PMTYVVSGLR 720
50 QTISLSGHIG VEVKVLTGFL LAFMVLSLLI YRPKKTV 757

<212> Type : PRT
<211> Length : 757
SequenceName : SEQ ID 378
SequenceDescription :

55 Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
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65 SKMSGSEIIS AINLDRSGVK ITGKNITLDG NSYISNAVIK DAHIANMDAG KINTGYLNAN 360
RIATEAITGE KIKMDYAFFN KLTANEGYFR TLFKADIFAT SVQSVTLAS KITGGVLAAT 420
NGASQWDLNN ANMTFNRDAT INFNSKNAL VRKDGHTAF VHFSNATPKG YRGSALYASI 480

GITSSGDGID SASSGRFAGL RSFRYATGYN HTAAVDQTEL YGDNVLIADD FSINRGFKFR 540
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<212> Type : PRT
5 <211> Length : 594
SequenceName : SEQ ID 379
SequenceDescription :

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<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
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15 ITKDINKSTN LTLALNNAFL ASGASSEAS RGLEQYQML SAGKVDMQAW KTLQETMPYA 180
LQQTAEAFGF AGASAQKDFY EALKNGQITF DQFSNKLIEL NDGVGGFAEL AKENSKGIET 240
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TTIKTVTAVQ AVSTTMTKAD MVARLSQLGV LKASTVIYGV MTGAISLSTA ATIASTAAPT 420
20 ALKAALVALT GPVGWVVGAI GALVAVGVSL WSWLTKESE TKKLKKEQEG LVESNKQLRD 480
SVREGVQERK KLESVKEST AAHQKLADI IKLAAKENKT AGEKQNLKKN IDQLNGSIDG 540
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KKWNEBANVS DSVRKEKIAE LTEEEAKLKN MQTQLQEEYN KTSATQAAAA DAMAAEESG 660
SARQVIAYEN MSEAQRTAID NMRTKYSLEL ETTTSIFDAI EQKTALSVDQ MNTNLEKNRA 720
25 ATEQWATNLE ILAQRGVDDG ILEQLRRMGP EGATQTQVFF DATDAELAPL QENFRAATET 780
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IAARITATIQ SALDIHSPSR VMRDEVGRFI PQGIAVGIDA DRKVIDSSMQ KLKESMTINA 1020
30 TPEIASGFGG GVAGIANQTT NNSNNSFTLN VKVDESDGNS HEKYQRLFRE FSWYIQQQQG 1080
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<211> Length : 1086
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35 SequenceDescription :

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<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
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<212> Type : PRT
45 <211> Length : 158
SequenceName : SEQ ID 381
SequenceDescription :

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<400> PreSequenceString :
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55 SLNKIGRQIN HLKTYGVPV STETNKDEAT GEETTTTVQP SAQQNANYKQ QLQDLNDAYA 180
DAQAEVNKAQ IALNDTVVIS SVSGTVVEVN NDIDPSSKNS QTLVHVATEG QLQVKGLTE 240
YDLANVKVGQ SVKIKSKVYS NQEWTKISY VSNYPESNA GSTTPAGSTG AGSSTGAAYD 300
YKIDIISPLN QLKQGFVSV EVVNEAKQAL VPLTAVIKK KKHVWYD ATGKAKKVEV 360
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SequenceDescription :

65 Sequence

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5  QSGNWWGYGAS MRMFPPESGF DFSTTTEPVC TPA.SNPIKQR GAIGIINFAR RIGGLSLGAN      180
   LKAGFRDAQG LQHTSVSSDI GLQWVGNVAK SFTSEEPNLY IGLAATNLGL TVKVSDKIEN      240
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   FLFSLGATTS MNVQTLASSD AKSLYQNLAY SIGAMFDPFS FLSLSSSFRI NHKANMRVGV      360
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10 <212> Type : PRT
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        SequenceName : SEQ ID 383
        SequenceDescription :

15 Sequence
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<400> PreSequenceString :
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   GSNYYFSVPI TVNPTYTFAV GRWRIPLSLG VGLNIQSYLS KKAPGLIAEA SAGLYYQYTP      180
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<212> Type : DNA

<211> Length : 4716

SequenceName : SEQ ID 386

SequenceDescription :

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<212> Type : DNA

<211> Length : 2916

SequenceName : SEQ ID 387

45 SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
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SequenceName : SEQ ID 388
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<212> Type : DNA

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SequenceName : SEQ ID 389
SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7

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<211> Length : 4254

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SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
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SequenceDescription :

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25 <211> Length : 564
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SequenceDescription :

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    agcgccactc ttgatcagtg gaacggtaaa gactctcata tgacagttaa acaattcggg 360
55  ggcggcaacg gtgcagcggg tgaccagact gcatctaatt ccaccgtcaa cgtaactcag 420
    gttggctttg gtaacaacgc gaccgctcat cagtactaa 459
    <212> Type : DNA
    <211> Length : 459
    SequenceName : SEQ ID 403
    SequenceDescription :

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60  Sequence
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    <213> OrganismName : Escherichia coli O157:H7
    <400> PreSequenceString :
65  atgcctattg gtaatcttgg tcataatccc aatgtgaata attcaattcc tcctgcacct 60
    ccattacctt cacaaaccga cgggtgcaggg gggcgtgggt agctcattaa ctctacgggg 120

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```

ccgttgggat  ctctgtgcgt  atttacgcct  gtaaggaatt  ctatggctga  ttctggcgac  180
aatcgtgcca  gtgatgttcc  tggacttcct  gtaaatccga  tgcgcctggc  ggctgtctag  240
ataaacttga  atgatggatt  tgaagtctct  catgatcatg  gtccgctcga  tactcttaac  300
aggcagattg  gctcttcggt  atttcgagtt  gaaactcagg  aagatggtaa  acatattgct  360
5  gtcggtcaga  ggaatggtgt  tgagacctct  gttgttttaa  gtgatcaaga  gtacgctcgc  420
ttgcagtcca  ttgatccctga  aggtaaagac  aaatttctat  ttactggagg  ccgtggtggt  480
gctgggcatg  ctatggctac  cgttgcttca  gatatcacgg  aagcccgcca  aaggatactg  540
gagctggttag  agcccaaagg  gaccggggag  tccaaagggt  ctggggagtc  aaaaggcgtt  600
ggggagttga  gggagtcaaa  tagcgggtgc  gaaaacacca  cagaaactca  gacctcaacc  660
10  tcaacttcca  accttcgttc  agatccctaa  ctttgggttg  cggtggggac  tgttgctaca  720
gggtctgatag  gggtggcgcc  gacgggtatt  gtacaggcgc  ttgcattgac  gccggagccg  780
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15  caggctaaag  cagcaggcga  agaggccaaa  cagcaagcca  ttgaaaataa  tgctcaggcg  1020
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gctggctacg  gtcttagtgg  cgcattgatt  cttggtgggg  gaattggtgt  tgccgtcacc  1140
gctgcgtctc  gcctgcaaaa  tcagccggta  gaacaaacaa  caacaacaac  tactacaact  1200
acaactacaa  gcgcacgtac  ggtagagaat  aagcctgcaa  ataatacacc  tgcacagggc  1260
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25  cgtctggcgc  taagtgtgtg  attacgccat  gacatgggag  gattaacggg  ggggagtaat  1620
agcgtctgtg  atacttcgaa  taaccaccca  gcgcgggat  cccatcgttt  cgtctaa  1677

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<212> Type : DNA

<211> Length : 1677

30 SequenceName : SEQ ID 404
SequenceDescription :

Sequence

35 <213> OrganismName : Escherichia coli O157:H7

<400> PreSequenceString :

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atggctgcgc  ctacagtcac  ttttcagggg  gaagtaaccg  atcagacctg  ttccgtaaat  120
atcaacggtc  aaaccaattc  agtagtattg  atgccgaccg  tagccatggc  tgacttcggg  180
40  gcaactttag  ctgatggtca  gagcgcaggc  cagacgccgt  ttacggtttc  tgtgtctaac  240
tgccaggctc  caactgggtc  agatcaggca  atcaacacca  ccttcctggg  ctacgacgtt  300
gacgctagca  cgggtgttat  gggaaaccgt  gataccagca  gcgatgcggc  gaaaggcttt  360
ggcattcagt  taatggattc  cagcacttct  ggtaaccag  taactctggc  tggcgcgact  420
aacgtaccgg  gtctgaccct  gaaagtgggc  gataccgaag  ccagctacga  cttcgggtgc  480
45  cgttacttcg  ttatcgatag  cgctgctgcc  actgccggta  aaattaccgc  tgtcgcagaa  540
tacacctga  gctacctcta  a
561

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<212> Type : DNA

<211> Length : 561

50 SequenceName : SEQ ID 405
SequenceDescription :

Sequence

55 <213> OrganismName : Escherichia coli O157:H7

<400> PreSequenceString :

```

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aacaatggcc  tgatgacgtt  caacgcgacg  ctgggcggcg  ataattcacc  caccgataag  120
atgaacgtga  aaggcgatac  ccaagggaac  actcgcgttc  gggttgataa  cattggcggc  180
gtcgggtcgc  aaacgggtcaa  cgggtattgaa  ctcataggag  ttggcggtaa  ttctgcaggg  240
60  aatttcgcgc  tgaccaccgg  aactgtcgaa  gctggggcct  acgtctacac  gctggctaaa  300
gggaagggga  atgacgagaa  aaactgggat  ctgaccagta  aatgggacgg  cgtaacgcca  360
gcggatacac  ccgataccat  caataatccc  cctgttgttg  atccggaagg  cccatcagtt  420
tatcgcccg  aggcgggaag  ctatatcagc  aacattgccg  cagccaactc  gctgttttag  480
catcgcttac  acgaccgtct  gggtagccg  caatatacag  attcactgca  ttctcaggat  540
65  tcagcaagca  gtatgtggat  gcgtcatgtc  ggggggcacg  aacgttccag  tgccggagac  600
ggccagctaa  atactcaggc  taaccgctat  gtattgcagc  taggcggcga  tttggcgacg  660
tggagttagc  acgcgcagga  tcgtggcat  cttggcgtag  tggcaggcta  cgccaatcag  720

```

```

cacagtaata ctcagagtaa tcgtgtgggt tataaatcgg atggggcgcat cagcggttac 780
agcgctgggc tgtacgcgac ctgggtatcag aacgatgcga ataagaccgg cgcttatgtt 840
gacagctggg cgctgtataa ctgggttgat aacagcgtca gttccgataa ccgttctgct 900
gacgactatg attctcgcgg tgtgacggcc tctgttgagg gtgggtatac ctttgaagcg 960
5 ggaacatgta gcggcagcga agggacgctg aatacctggg acgtccagcc acaggcgcaa 1020
atcacctgga tgggtgtgaa agattctgac catgcccggg aagacggaac gcgcattgaa 1080
acggaaggcg acggaacgt gcaaacgcga cttgggggtg aaacctacct gaatagccat 1140
caccagcgtg acgatggtaa acagcgtgag ttccagcctt acattgaagc gaactggatc 1200
aacaatagca aagtctacgc cgtgaagatg aatgggtcaa ccgtaagccg tgatgggtgcg 1260
10 cgaaatctcg tgaagtagc taccgggggtt gagcggaag taaataacaa ccttagcctg 1320
tgggggaatg tcggtgtgca actaggtgat aaaggctata gcgatactca gggcatgctg 1380
ggagtgaat atagctggta a 1401

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<212> Type : DNA

<211> Length : 1401

15 SequenceName : SEQ ID 406

SequenceDescription :

Sequence

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20 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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catcgttttg ctggtttttt tgtccggctc tttgtgcct gtgcttttgc cgtacaggca 120
cctttgtcat ctgcogaact ctattttaat ccgcgctttt tagcggatga tccccaggct 180
25 gtggccgatt tatcgcgttt tgaaaatggg caagaattac cgccagggac gtatcgcgtc 240
gatattctatt tgaataatgg ttatatggca acgctgatg tcacatttaa tacggcgac 300
agtgaacaag ggattgttcc ctgcctgaca cgcgcgcaac tcgccagtat ggggctgaat 360
acggcttctg tcgcgggtat gaatctgctg gcggatgatg cctgtgtgcc attaacaca 420
atggtccagg acgctactgc gcatttagat gttggtcagc agcactgaa cctgacgatc 480
30 cctcaggcat ttatgagtaa tcgcgcgctt ggttatattc ctctgagtt atgggatccc 540
gggtattaatg ccggattgct caattataat ttacgcgga atagtgtaca gaatcggatt 600
gggggtaaca gccattatgc atattttaac ctacagagtg ggttaaataat tgggtcgtgg 660
cgtttacgcg acaataccac ctggagttat aacagtagcg acagatcatc aggtagcaaa 720
aataaatggc agcatatcaa tacctggctt gagcgagaca taataccgtt acgttcccgg 780
35 ctgacgctgg gtgatggtta tactcagggt gatattttcg atggtattaa ctttcgcggc 840
gcacaattgg cctcagatga caatatgtta ccgatagcc aaagaggatt tgcccgggtg 900
atcccggtga ttgctcgtgg tactgcacag gtcactatta acaaaatgg gtatgacatt 960
tataatagta cgggtgccgc ggggcctttt accatcaacg atatctatgc cgcaggtaat 1020
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40 ccctattcgt cagtcggctt tttgcaacgt gaagggcata ctcgttattc cattacggca 1140
ggagaatacc gtagtggaaa tgcgcaacag gaaaaaccc cgtttttcca aagtacatta 1200
ctccacggcc ttccagctgg ctggacaata tatggtggaa cgcaactggc agatcggtat 1260
cgtgctttta attttggtat cgggaaaaat atgggggcac tgggcgctct gtctgtggat 1320
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45 tttctctata acaaatcgct caatgagtc ggcagcaata ttcagttagt ggggtaccgt 1440
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aacatcgaaa cacaggacgg agttattcag gtttagccga aattcaccga ctattacaac 1560
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tcaacactgt atttgagtgg tagccatcaa acttattggg gaacgagtaa tgcgatgag 1680
50 caattccagg ctggattaaa tactgcgttc gaagatatca actggacgct cagctatagc 1740
ctgacgaaaa acgcctggca aaaaggacgt gatcagatgt tagcgcgtaa cgtcaatatt 1800
cctttcagcc actggctgcg ttctgacagt aaatctcagt ggcgacatgc cagtgccagc 1860
tacagcatgt cacacgatct caacggtcgg atgaccaatc tggctggtgt atacggtagc 1920
55 ttgctggaag acaacaacct gcgctatagc gtgcaaaccc gctatgccgg gggaggcgat 1980
ggtaatagcg gaagcacagg ctacgccacg ctgaattatc gcggtgggtta cggcaatgcc 2040
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60 gataccaata ccctggctga taacgtcgat ttagataacg cggtcgctaa cgttgttccc 2340
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cagagtagcg gcattgttgc ggataatggt cagggtttacc tcagcggaat gcctctagcg 2520
ggaaaagtgc aggtgaaatg gggagaagag gaaaatgctc attgtgtcgc caattatcaa 2580
65 ctgccaccag agagtcagca gcagttatta acccagctat cagctgaatg tcgttaa 2637

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<212> Type : DNA

<211> Length : 2637
SequenceName : SEQ ID 407
SequenceDescription :

5 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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10 atgcagataa tctttggaga aaaatgcgtg tcattactac gactattttt tgccgcgctc 60
   ttaatgctat ggtgcgctca aaccgctgct tatagcgggc agtgtcatac cactcagggg 120
   aatccgtata ttggcgctcaa ttttggcggt aaaaccctgg aggaagaaga aaatacgact 180
   ggggtagtaa aagacaaatt ttatcagtggt aacgaatcga atgattatta tgtttcctgt 240
   gattgcgata aagacaatgt cagaagtggc cgatgggcat tcgccgcgga ttcaccgtta 300
   gtctatttag gcgacaactg gtacaaaatt aatgactatc ttgccgcca . agttttattg 360
15 cagggttaaag gcagttctcc tacagcggtt cctttcgaaa acgtggggac tggggcagat 420
   acccggtggc atattttgtga ccccgcggtt caacgttttag gcggccaggg agctagcggg 480
   aatagcggta gcttttccct gaaaatattg cagccgttcg ttgggtcggg cgtcattcct 540
   cctatggcgc tggcgcgatt atttgaatgc tacaacatac ccgcagggtga ttcctgcacg 600
   actacaggca caccggtttt agtgtattac ctgtctggta ctatcaattc acttggctca 660
20 tgttcctgca atgccggaga aacaatcgag gtcgatctgg gcgacgtatt tgcggctaac 720
   tttcgtggtt tagggcataa gcctcttggg ccagaaacgg cagaacttgc aattccagtc 780
   aggtgtaaca cgggaaacgc ggggttagtt aacgtcaacc tgagtctgac ggcaaccaca 840
   gacccagct atccccaggc gattaagacg tcacgtcctg gcgtggcggt ggtggtgacc 900
   gatagccaga acaacattat ttcccttgcg ggtggaacat taccgctctc tattcctgat 960
25 gatgcagaca gtatcgcggtg a
```

<212> Type : DNA
<211> Length : 981
SequenceName : SEQ ID 408
SequenceDescription :

30 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

```
35 atgaaaaatta aaactctggc aatcgttggt ctgtcggctc tgtccctcag ttctacagcg 60
   gctctggccg ctgccacgac gggttaatggt gggaccgctc actttaaaagg ggaagttytt 120
   aacgcgcgtt gcgcagttga tgcaggctct gttgatcaaa ccggttcagtt aggacagggt 180
   cgtaccgcat cgctggcaca ggacggagca accagttctg ctgtcgggtt taacattcag 240
   ctgaatgatt gcgataccaa tgttgcatct aaagccgctg ttgccttttt aggtacgggtg 300
40 attgatgcgg gtcataccaa cgttctgggt ctgcagagtt cagctgcggg tagcgcaaca 360
   aacgttgggt tgcagatcct ggacagaacg ggtgctgcgc tgacgctgga tgggtgcgaca 420
   ttcagtgagc aaacaacctt gaataacgggt actaacacca ttccgttcca ggcgcggtat 480
   tatgcaatcg gcgaggcaac cccgggtgct gctaattgcg atgcgacctt caagggttcag 540
   tatcaataa
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<212> Type : DNA
<211> Length : 549
SequenceName : SEQ ID 409
SequenceDescription :

50 Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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55 atgaaattaa aagtcacgcg tacactgatt gctactgttg ccgtgggtgt aagctttaac 60
   agcaattttg cttctgcgag tacaacgtcc gcttctttaa ccgtaaacag taacctgact 120
   atgggtacct gcagtgctca gataatggat aatagtaata aagtgtatcaa tgaagtgggtc 180
   tttggcaatg tttatatattc tgaactcggg gcaaaaagca aagtgcaca gtttaaaatt 240
   cgcttttagca attgctctgg ccttcccca aacagcgccc aaatagtgtt ggcacctaat 300
   ggtatctcct gtgctggttc tcaatcgtca tcggcgggtt tttctaaca gtttactgac 360
60 gctagcgcag caaccagaac ggctgtggaa gtatggacta cagatacacc ggaaggaat 420
   ggcagtacgc aatttcattg tgctcaaaag ataccagtgc ctgtgacgct tcccgcgac 480
   accacaactc agccttacga ttaccgtta atgtgcaggg tgaccgttgc ggaaggtaga 540
   ttggtaacgg atgtaagacc gggtaatttc cgctctccca cgactttcac gatcacttat 600
   cagtaa
```

<212> Type : DNA
<211> Length : 606
SequenceName : SEQ ID 410

SequenceDescription :

Sequence

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5  <213> OrganismName : Escherichia coli O157:H7
   <400> PreSequenceString :
   ttggcatcaa cagttgagta tggtagagaca gttgatgggtg ttgtcctgga aaaagatatac 60
   cagctggttt atgggaccgc caataatacag aaaatcaatc ctggcggaga acagcatatt 120
   aaagaatttg gtataagtag taatactgaa attaacggcg ggtatcagta cattgaaatg 180
10 aatggcaccg cagaatactc agtattaaat gatggtttatc aaattgttca aatgggtggc 240
   ggggcaaac agactacgct caataatggt gtgtacagg tttatggcg agcgaatgat 300
   cccacgatta aaggcgggcg cttaatcggt gaaaaagatg ggattaccgt ccttgccgct 360
   atcgaaaagg gaggattact ggaggttaa gaggggggat tagcgattgc ggtagatcag 420
   aaagcaggcg cgaattattaa agcaagcacg cgggtcatgg aggtattcgg aacaaaccgt 480
15 ctcggtcagt tcgaaatcaa gaatggtatt gctaacaata tgctgttgg aaacggcggg 540
   agtttgcgag ttgaagaaaa tgacttcgct tataatacta ctgtagatag tggcggctta 600
   ctggagggtta tggatggcgg gactgcaact ggcgttgata aaaaagcagg cggaaaatta 660
   attgtctcaa cgaatgcgct ggaagtgaat ggtacaaaca gtaaggcca atttagtata 720
   aaagatgggtg tgtcaaaaaa ttatgaactg gatgatgggt cggggttat tgttatggag 780
20 gacacgcagg ccattgacac tatcctcgat gacgatgcca ctatgcaatc gctgggaaag 840
   gatactggta cgagagtgc ggcaaatgcg gtatatgatc tcggtcgatc agatcagaat 900
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   gaggttatga agcgcgcaat aaattatgca ccgcgaatgt tgggtgggtaa ggtagtgggt 1080
25 tctgaggggc ctctcttaag aacgcattggt gccgtggata ccagcaaagc ggatgtttcg 1140
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   cttaacttag ccaaccttgc gatgtctggc gcaaatgtga ttatgatgga tgagtcagtg 1260
   actcgttcat ctgtgacggc aagtgcggaa aatttcaacta cgttgaccac caataccctg 1320
   tcgggaaacg gcaattttta tatgctgacc gatatggcga atcatcagag cgatcagctc 1380
30 aacgtcaccc gcgcattgac aggtgatttc aaaatattcg tgacggacac cggtgccagc 1440
   ccggcagcag gagatagcct tacactggta acaacgggcg gcggtgatgc tgcatttacg 1500
   ttgggcaatg ccggaggcgt tgttgatata ggtacgtatg aatatacctt gctggataat 1560
   ggtaaccata gctggagctc ggcagagaat cgcgcgcaaa ttacccttc aaccactgat 1620
   gtgctgaata tggcggccgc acaaccgctg gtatttgatg cagaactgga caccgtgcgt 1680
35 gagcgtcttg gtacgtaaa aggcgttagt tacgatacgg cgatgtggag ttcggcaatt 1740
   aacaccgcga acaacgtgac cactgatgcg ggagctgggt ttgagcaaac attgacgggc 1800
   ctgacgctcg gtatcgatag ccgtttctcc cgtgaagaaa gcagcacaat tcgcggttg 1860
   ttctttgggt actctcattc tgatattggt tttgatcgcg gcggcaaaagg caatgtcgat 1920
   agctataccc tgggggctta tgccgggttg gagcatcaga acggtgccta tgttgatgga 1980
40 gtggtgaaag ttgaccgttt tgccaacacc atccatggca agatgagtaa tggggcaaca 2040
   gcgtttggcg attacaatag taacggcgcg ggtgctcatg tcgagagcgg gttccgttg 2100
   gttgacggat tgtgagtggt tagaccctat ctggccttta cggcctttac cacagatgg 2160
   caggactaca cgttatcaaa cggcatgcgc gcggatgtgg gaaatacccg gatattacgc 2220
   gctgaagcgg gaacggcggg aagctatcac atggacctgc aaaacgggtac gacgctggaa 2280
45 ccctggctga aagccgcgct gcgtcaggaa tacgccgatt ctaaccagg gaaagttaat 2340
   gacgatggca aatttaataa tgatgtggct ggaaccctg cgttttatca ggctgggata 2400
   aggtcatcgt ttaccccgac gttaaagggt catttgtcag tcagctatgg caatggcgca 2460
   ggggtagaat cgccgtggaa taccaggcg ggtgtggtct ggacgttctg a 2511

50 <212> Type : DNA
   <211> Length : 2511
       SequenceName : SEQ ID 411
       SequenceDescription :

55 Sequence
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   <213> OrganismName : Escherichia coli O157:H7
   <400> PreSequenceString :
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   accacatcct ggtatgcatt ggcaaatgaa tgttatatag agagaaatgc tgaaggggat 120
   tatcacatga agataagctc tactcagctt agtctggcgt cacaaatggt cgagggtccg 180
   acagaaatag ccgaagctac atgggatgta aatattcaac taagaggcga tgccataggg 240
   tgtaaatctc ttggggatag taaggcagtt cactttctta atacagctga cccaagttaa 300
   atatccacgt acaccacaac gaatggcgca gcgttattaa aaacaactgt tccaggcatt 360
65 gtgtattctg tcgagttatt atgccttagt tgtggtgccg cagatgaact tgatttatgg 420
   ctacctgcac aaagtggcg agataacttc ataccaagca ccagacgaa atgggcctat 480
   gagtacagtg atcaaaagttg gtatttacgt tttcgcttat tcataactcc tgaatttaaa 540

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      cccaagaatg gtgtttccag cggaacaacg atagcaggaa agattgcgtc atggtatata      600
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      gtcgatgaac cgacttgtgc aacagttgcc ctggcacaag atcagggcaa cgtcagtggtc      720
      aatcaggtaa cgcttgggaa cagctatgtt tcggaagtga aaaatgggct tacgcgggaa      780
5      atcccttttt ctatccgtgc tgaatactgt tatgccagta aaattacggg taagttgaaa      840
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      SequenceDescription :

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Sequence

5 <213> OrganismName : Escherichia coli O157:H7
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15 <212> Type : DNA
<211> Length : 531
SequenceName : SEQ ID 414
SequenceDescription :

Sequence

25 <213> OrganismName : Escherichia coli O157:H7
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ccagaacaga acaatatattt gccttactcc gctcgtctga agtcaactca gaagtccgtc 480
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<211> Length : 531
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SequenceDescription :

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40 <213> OrganismName : Escherichia coli O157:H7
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55 SequenceName : SEQ ID 416
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Sequence

60 <213> OrganismName : Escherichia coli O157:H7
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<212> Type : DNA
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5 SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
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gttactgata cttttgctga agtttagcga actgctgtcg gtttactgcc gaaagagttc 240
15 atgattttctg ttgagtgtga tccaggtgct ccgaagaatg ctgagttaac tatgggttct 300
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<211> Length : 597
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25 SequenceDescription :

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35 gaaaccttta agtccgccgc aattcgtttc gatggtaatg aagatgctca tggtaatggc 300
aacctggcaa ttggtacccc gctggataac tctaacgatg ctgccgctgg tattagcccg 360
agtataaca gtgggataa tactggtgcg ggtgccgtta gtgcagcgaa aggcgtagct 420
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<212> Type : DNA
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SequenceName : SEQ ID 419
45 SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
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55 aaaagcgaac tgaataacga tcgcgatagc cagggacaat cttatcgttt cttatatctc 300
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<212> Type : DNA
10 <211> Length : 1458
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    SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7

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<212> Type : DNA

<211> Length : 531

SequenceName : SEQ ID 423

15 SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7

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60 aaatcccgca tggcagatgg ttcggaactg ccaatgggag ccgatgtgct ggatgagaat 2340
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aaaggccact tgtcagttcg ctggggtgaa ggtgctaacc atagctgcca attgcccttt 2460
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<212> Type : DNA

65 <211> Length : 2523

SequenceName : SEQ ID 424

SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
 5 <400> PreSequenceString :
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 cagttgccca aaggtacggc tccactcacg ctaaattttg accagcagtg ctggcagcct 180
 gcagatgcga taaaactcaa tcagatgctt tccctgcaac cttgtagcaa cagcccgctt 240
 10 caatggcgat tggttcaggga cggcaaatat acgttgcaaa tagaoaccgg ctccggtacg 300
 ccaacattga tgatttccat ccagaacggc gccgaaccgg tagcaaacct ggtccgtgaa 360
 tgcccgaat gggatggatt accgctcacg ctggatgtca gcgccacttt ccggaaggaa 420
 gccgcccgtac gggattatta cagccagcaa attgcatag tgaagaacgg tcaaataacg 480
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 15 tctgcccctt tcgactggca taacgccacg gtttactttg tgctgacaga tcgtttcga 600
 aacggcgatc ccagtaataga ccagagttac ggacgtcata aagacgggtat ggcggaaatt 660
 ggcacttttc acggcgcgga tttacggcgc ctgaccaaca aactggatta cctccagcag 720
 ttggcggtta atgctttatg gataagcgcc ccatttgagc aaattcacgg ctgggtcggc 780
 ggcgggtacaa aaggcgattt ccgcatttat gcctaccacg gttattacac acaggactgg 840
 20 acgaatcttg atgccaatat gggcaacgaa gcgatctac ggacgctggg tgatagcgca 900
 catcagcgcg gtattcgtat tctctttgat gtcgtgatga accacaccgg ctatgccacg 960
 ctggcggtata tgacaggata tcagtttggc gcgttatatc tttctgggtg cgaagtga 1020
 aaaacgctgg gtgaacgctg gagcgactgg aaacctgccg ccgggcaaac ctggcatagc 1080
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 25 tggatccgta ccgatatcgg cgattacgac aatcctggat tcgacgatct caccatgtcg 1200
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 30 cttcgcgat tgaaaaaagc taaccccgac aaagcattag atgacaaacc tttctggatg 1500
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 35 ctattagcgc caggcgcggt acaaatcttt tatggcgatg aatcctcgcg tccgttcggg 1800
 cctacaggtt ctgatccgct gcaaggatca cgttcggata tgaactggca ggatgttagc 1860
 ggtaaatctg ccgccaacgt cgcgcactgg cagaaaatca gccagttccg cgcccgccat 1920
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<212> Type : DNA
 <211> Length : 2031
 SequenceName : SEQ ID 425
 SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
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 gaagagtatt atttcgaccc cattatgctg gaaaccacaa aaagtgggtat gcaaaacacc 180
 gatctgtcac gtttttcaaa aaaatacgca caactaccag gaacttatca ggttgatatc 240
 55 tggctgaata aaaagaaggt ttcacagaaa aaaattacat ttaccgcaaa tgcagagcaa 300
 cttctgcagc cacagtttac ggtagaacaa ctacgtgagc tgggtattaa ggtggatgaa 360
 atcccggcgc tggctgaaaa agatgacgat agcgtgatca actcgttga acaaatcatt 420
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 ccaacgctgt ttaccaacta ctcgtttaca ggttctgata accgttaccg ccagggcaat 600
 60 cgtagccaac gacagtacct aaatagcaa aatgggtgca attttggccc ctggcgatta 660
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 65 gcaatcgtga ctatcaggca aaatgggtat gtgatctatc aaagcaacgt gccagcgggt 960
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5  cagcgacctg ggcattctaaa atatagcgcg accgctggac gctatcgcg tgatgcaaac 1140
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   tttacgctgt atggcgccct gctcgggtct gaagattatt atgcgctggg gatcggtatc 1260
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   ttcgataacc agcactcttt tcatggctat caatggcgta cgcagtacat caaagatatt 1380
   ccggaaacca acaccaatat cgctgtcagc tactatcgct ataccaacga tggctatttt 1440
   agttttgatg aagccaatac ccgcaattgg gactataaca gtcgccaaaa aagtgaattt 1500
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   caagactatt ggggcaataa cgagaaaaac aggaatatct ctggtggggt ttccggccag 1620
10 caatggggaa ttggttacag cctgaattat caatacagcc gctacactga tcaaaataat 1680
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20 ggtgcaatgg tagcggcgcg tttcaacgcc aatatcggtt atcgcgta ctgttacagtc 2280
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   caaagctgga ctgtacgctg gggaaatcag gcagatcaac aatgtcagtt tgcttttagt 2460
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<212> Type : DNA

<211> Length : 2517

SequenceName : SEQ ID 426

SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7

<400> PreSequenceString :

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   gcgaatgaaa cttccttttag taaaagtgtc gtgtttactg ggatatcttg tgatacgagc 180
   acggataaaa tagtttataa aaatatccaa agtgattggg ttgaagttgg gccttttggg 240
   aatggcgaaa aattaaagg taaaatagag tctttaggta aaaccagcga cacaattggg 300
40  aaatccagca atgcgcaggg agtattacct tatgtgtgta aaatagccag aggcacacct 360
   gattttactg gagaagaaaa atctacctgg tttatttcag ataccgtgat tgcaaatatt 420
   ggcggtgagt catcgtcctc catcgatttt ttggtgggta tttgtaaggc attgaagttt 480
   aactgggtgtg tgaattatct caccagcaaa ctggcggggg atacatttac gcttgggtta 540
   aatatttctc attatcctaa aaatacgacc tgtaagcctg aaaacaccgt tataaaagta 600
45  gatgatatcg ccttgttcca gtcagaaat cagggaagaa ttgcggcgaa cagtaaggaa 660
   ggaacaatta cgttgaaatg tgataatctt ttgcgggaca aaaaacaagc atcgcggaat 720
   atgggtgtat atctttctag cagtgaacta gttaaaggaa gtaatactat tttgcgtggg 780
   aaaacagata atgggtgtag gtttgtgttg gatctaacag aaccacaaaa agggactgag 840
   gctgccatta aaatttcggc caacggcgat cagggcgcgg cgacatcatt atggaaaaa 900
50  gataaaccag gagtttcatt aaatagcaac attattaata taccagtcac ggccagttac 960
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<212> Type : DNA

<211> Length : 1035

SequenceName : SEQ ID 427

SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7

<400> PreSequenceString :

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   actgtgcttg caccaaccac cgttgtgacg cgtcaggata tcgaccgctg gcagtcgacc 180
65  tcggttaaat atgtgctgcg ccgtcttcgg ggcgtcgata tcacccaaaa cggcggttca 240
   ggtcagctct atctattttt tattcgcggt acaaatgccg gtcagtgtgt ggtgttaatt 300
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attgcgcttg tccagcgtgt tgaatatatc cgtggggccac gctccgcctt ttatggttcc 420
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5 gttgcctatg gtaataccgg aacgcaagcg cagccagata acgatgggtt tttaagtaaa 660
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20 tatgattatg tcatgacgcg caatgcaatt accgacacgc cgttggttac ccgtgctaaa 1560
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gttcgtggta aaatagccaa cctgttcgac aaagattatg agacagtcta tggctaccaa 1800
25 actgcaggag gggaatacac cttgtctggc agctacacct tctga 1845
<212> Type : DNA
<211> Length : 1845
SequenceName : SEQ ID 428
SequenceDescription :

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Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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tcttcattta atcaggcagc cataattggt caagctggga ctaataatag tgctcagtt 180
ggcaggggag gtcacaaaact tttggcgggt gttgcgcaag aaggtagtag caaccgggca 240
aagattgacc agacaggaga ttataacctt gcataatatt atcaggcggg cagtgcgaat 300
40 gatgccagta ttgcgcaagg tgcttatggt aatactgcga tgattatcca gaaaggttct 360
ggtaataaag caaatattac acagtatggt actcaaaaaa cggcaattgt agtgcagaga 420
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<212> Type : DNA
<211> Length : 456
SequenceName : SEQ ID 429
SequenceDescription :

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50 <213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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accatccagt tgcgaaatac cagcgatcag ccctatatca ttaatatcca tgttgaggat 180
55 gaacgtgggt ctgacaagaa tgtaccgttt atgccaaccc cgcagacatt tcgcatggaa 240
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gagtcgtgtt tctgggttag tttcagtcaa ctaccttatc tgaataagaa tgataaaagt 360
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60 attgaagtga cgaatcccac gggtatttac gtcacaattc gcgcgcgtga actgcttaat 540
aatggtaaaa aagtccccct cgcgaattcg gtaattgatt ctctctaaag cacaactgaa 600
tggacactac cctctggcat cagtgtcgct cccggtgcgc agatccattt agtgaccgtc 660
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<212> Type : DNA
65 <211> Length : 702
SequenceName : SEQ ID 430
SequenceDescription :
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